

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problems Mailbox.**

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Choi et. al.

(ii) TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

(iii) NUMBER OF SEQUENCES: 452

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.  
(B) STREET: 9410 Key West Avenue  
(C) CITY: Rockville  
(D) STATE: Maryland  
(E) COUNTRY: USA  
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
(B) COMPUTER: HP Vectra 486/33  
(C) OPERATING SYSTEM: MSDOS version 6.2  
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Unassigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/961,083  
(B) FILING DATE: OCT-30-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Michelle S. Marks  
(B) REGISTRATION NUMBER: 41,971  
(C) REFERENCE/DOCKET NUMBER: PB340P2C1

(vi) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504  
(B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1999 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

09/65272 "012201

Sub

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TAAAATCTAC	GACAATAAAA	ATCAACTCAT	TGCTGACTTG	GGTTCTGAAC	GCCGCGTCAA	60
TGCCCAAGCT	AATGATATTC	CCACAGATTT	GGTTAAGGCA	ATCGTTTCTA	TCGAAGACCA	120
TCGCTTCTTC	GACCACAGGG	GGATTGATAC	CATCCGTATC	CTGGGAGCTT	TCTTGCGCAA	180
TCTGCAAAGC	AATTCCCTCC	AAGGTGGATC	AACTCTCACC	CAACAGTTGA	TTAAGTTGAC	240
TTACTTTTCA	ACTTCGACTT	CCGACCAGAC	TATTTCTCGT	AAGGCTCAGG	AAGCTTG GTT	300
AGCGATT CAG	TTAGAACAAA	AAGCAACCAA	GCAAGAAATC	TTGACCTACT	ATATAAATAA	360
GGTCTACATG	TCTAATGGGA	ACTATGGAAT	GCAGACAGCA	GCTCAAAACT	ACTATGGTAA	420
AGACCTCAAT	AATTTAAGTT	TACCTCAGTT	AGCCTTGCTG	GCTGGAATGC	CTCAGGCACC	480
AAACCAATAT	GACCCCTATT	CACATCCAGA	AGCAGCCCAA	GACCGCCGAA	ACTTGGTCTT	540
ATCTGAAATG	AAAAATCAAG	GCTACATCTC	TGCTGAACAG	TATGAGAAAG	CAGTCAATAC	600
ACCAATTACT	GATGGACTAC	AAAGTCTCAA	ATCAGCAAGT	AATTACCCTG	CTTACATGGA	660
TAATTACCTC	AAGGAAGTCA	TCAATCAAGT	TGAAGAAGAA	ACAGGCTATA	ACCTACTCAC	720
AACTGGGATG	GATGTCTACA	CAAATGTAGA	CCAAGAAGCT	CAAAAACATC	TGTGGGATAT	780
TTACAATACA	GACGAATACG	TTGCCTATCC	AGACGATGAA	TTGCAAGTCG	CTTCTACCAT	840
TGTTGATGTT	TCTAACGGTA	AAGTCATTGC	CCAGCTAGGA	GCACGCCATC	AGTCAAGTAA	900
TGTTTCCTTC	GGAATTAACC	AAGCAGTAGA	AACAAACCGC	GACTGGGGAT	CAACTATGAA	960
ACCGATCACA	GACTATGCTC	CTGCCTTGGA	GTACGGTGTC	TACGATTCAA	CTGCTACTAT	1020
CGTTCACGAT	GAGCCCTATA	ACTACCCTGG	GACAAATACT	CCTGTTTATA	ACTGGGATAG	1080
GGGCTACTTT	GGCAACATCA	CCTTGCAATA	CGCCCTGCAA	CAATCGCGAA	ACGTCCCAGC	1140
CGTGGAAACT	CTAAACAAGG	TCGGACTCAA	CCGCGCCAAG	ACTTTCCTAA	ATGGTCTAGG	1200
AATCGACTAC	CCAAGTATTC	ACTACTCAAA	TGCCATTTCA	AGTAACACAA	CCGAATCAGA	1260
CAAAAAATAT	GGAGCAAGTA	GTGAAAAGAT	GGCTGCTGCT	TACGCTGCCT	TTGCAAATGG	1320
TGGAAC TTAC	TATAAACCAA	TGTATATCCA	TAAAGTCGTC	TTTAGTGATG	GGAGTGAAAA	1380
AGAGTTCTCT	AATGTCGGAA	CTCGTGCCAT	GAAGGAAACG	ACAGCCTATA	TGATGACCGA	1440
CATGATGAAA	ACAGTCTTGA	CTTATGGAAC	TGGACGAAAT	GCCTATCTTG	CTTGGCTCCC	1500
TCAGGCTGGT	AAAACAGGAA	CCTCTAACTA	TACAGACGAG	GAAATTGAAA	ACCACATCAA	1560
GACCTCTCAA	TTTGTAGCAC	CTGATGAACT	ATTTGCTGGC	TATACGCGTA	AATATTCAAT	1620
GGCTGTATGG	ACAGGCTATT	CTAACCGTCT	GACACCACTT	GTAGGCAATG	GCCTTACGGT	1680
CGCTGCCAAA	GTTTACCGCT	CTATGATGAC	CTACCTGTCT	GAAGGAAGCA	ATCCAGAAGA	1740

09765272.012201

TTGGAATATA CCAGAGGGGC TCTACAGAAA TGGAGAATTC GTATTTAAAA ATGGTGCTCG 1800  
 TTCTACGTGG AACTCACCTG CTCCACAACA ACCCCCATCA ACTGAAAGTT CAAGCTCATC 1860  
 ATCAGATAGT TCAACTTCAC AGTCTAGCTC AACCCTCCA AGCACAAATA ATAGTACGAC 1920  
 TACCAATCCT AACAATAATA CGCAACAATC AAATACAACC CCTGATCAAC AAAATCAGAA 1980  
 TCCTCAACCA GCACAACCA 1999

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Ile Tyr Asp Asn Lys Asn Gln Leu Ile Ala Asp Leu Gly Ser Glu  
 1 5 10 15  
 Arg Arg Val Asn Ala Gln Ala Asn Asp Ile Pro Thr Asp Leu Val Lys  
 20 25 30  
 Ala Ile Val Ser Ile Glu Asp His Arg Phe Phe Asp His Arg Gly Ile  
 35 40 45  
 Asp Thr Ile Arg Ile Leu Gly Ala Phe Leu Arg Asn Leu Gln Ser Asn  
 50 55 60  
 Ser Leu Gln Gly Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Leu Thr  
 65 70 75 80  
 Tyr Phe Ser Thr Ser Thr Ser Asp Gln Thr Ile Ser Arg Lys Ala Gln  
 85 90 95  
 Glu Ala Trp Leu Ala Ile Gln Leu Glu Gln Lys Ala Thr Lys Gln Glu  
 100 105 110  
 Ile Leu Thr Tyr Tyr Ile Asn Lys Val Tyr Met Ser Asn Gly Asn Tyr  
 115 120 125  
 Gly Met Gln Thr Ala Ala Gln Asn Tyr Tyr Gly Lys Asp Leu Asn Asn  
 130 135 140  
 Leu Ser Leu Pro Gln Leu Ala Leu Leu Ala Gly Met Pro Gln Ala Pro  
 145 150 155 160  
 Asn Gln Tyr Asp Pro Tyr Ser His Pro Glu Ala Ala Gln Asp Arg Arg  
 165 170 175  
 Asn Leu Val Leu Ser Glu Met Lys Asn Gln Gly Tyr Ile Ser Ala Glu  
 180 185 190  
 Gln Tyr Glu Lys Ala Val Asn Thr Pro Ile Thr Asp Gly Leu Gln Ser  
 195 200 205  
 Leu Lys Ser Ala Ser Asn Tyr Pro Ala Tyr Met Asp Asn Tyr Leu Lys

09765272.012201



210	215	220
Glu Val Ile Asn Gln Val Glu Glu Glu Thr Gly Tyr Asn Leu Leu Thr 225 230 235 240		
Thr Gly Met Asp Val Tyr Thr Asn Val Asp Gln Glu Ala Gln Lys His 245 250 255		
Leu Trp Asp Ile Tyr Asn Thr Asp Glu Tyr Val Ala Tyr Pro Asp Asp 260 265 270		
Glu Leu Gln Val Ala Ser Thr Ile Val Asp Val Ser Asn Gly Lys Val 275 280 285		
Ile Ala Gln Leu Gly Ala Arg His Gln Ser Ser Asn Val Ser Phe Gly 290 295 300		
Ile Asn Gln Ala Val Glu Thr Asn Arg Asp Trp Gly Ser Thr Met Lys 305 310 315 320		
Pro Ile Thr Asp Tyr Ala Pro Ala Leu Glu Tyr Gly Val Tyr Asp Ser 325 330 335		
Thr Ala Thr Ile Val His Asp Glu Pro Tyr Asn Tyr Pro Gly Thr Asn 340 345 350		
Thr Pro Val Tyr Asn Trp Asp Arg Gly Tyr Phe Gly Asn Ile Thr Leu 355 360 365		
Gln Tyr Ala Leu Gln Gln Ser Arg Asn Val Pro Ala Val Glu Thr Leu 370 375 380		
Asn Lys Val Gly Leu Asn Arg Ala Lys Thr Phe Leu Asn Gly Leu Gly 385 390 395 400		
Ile Asp Tyr Pro Ser Ile His Tyr Ser Asn Ala Ile Ser Ser Asn Thr 405 410 415		
Thr Glu Ser Asp Lys Lys Tyr Gly Ala Ser Ser Glu Lys Met Ala Ala 420 425 430		
Ala Tyr Ala Ala Phe Ala Asn Gly Gly Thr Tyr Tyr Lys Pro Met Tyr 435 440 445		
Ile His Lys Val Val Phe Ser Asp Gly Ser Glu Lys Glu Phe Ser Asn 450 455 460		
Val Gly Thr Arg Ala Met Lys Glu Thr Thr Ala Tyr Met Met Thr Asp 465 470 475 480		
Met Met Lys Thr Val Leu Thr Tyr Gly Thr Gly Arg Asn Ala Tyr Leu 485 490 495		
Ala Trp Leu Pro Gln Ala Gly Lys Thr Gly Thr Ser Asn Tyr Thr Asp 500 505 510		
Glu Glu Ile Glu Asn His Ile Lys Thr Ser Gln Phe Val Ala Pro Asp 515 520 525		
Glu Leu Phe Ala Gly Tyr Thr Arg Lys Tyr Ser Met Ala Val Trp Thr 530 535 540		
Gly Tyr Ser Asn Arg Leu Thr Pro Leu Val Gly Asn Gly Leu Thr Val		

09765272.012201

(2) INFORMATION FOR SEQ ID NO: 3:

(A) LENGTH: 1714 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

AAATTACAAT	ACGGACTATG	AATTGACCTC	TGGAGAAAAA	TTACCTCTTC	CTAAAGAGAT	60
TTCAGGTTAC	ACTTATATTG	GATATATCAA	AGAGGGAAAA	ACGACTTCTG	AGTCTGAAGT	120
AAGTAATCAA	AAGAGTTCAG	TTGCCACTCC	TACAAAACAA	CAAAAGGTGG	ATTATAATGT	180
TACACCGAAT	TTTGTAGACC	ATCCATCAAC	AGTACAAGCT	ATTCAGGAAC	AAACACCTGT	240
TTCTTCAACT	AAGCCGACAG	AAGTTCAAGT	AGTTGAAAAA	CCTTTCTCTA	CTGAATTAAT	300
CAATCCAAGA	AAAGAAGAGA	AACAATCTTC	AGATTCTCAA	GAACAATTAG	CCGAACATAA	360
GAATCTAGAA	ACGAAGAAAG	AGGAGAAGAT	TTCTCCAAAA	GAAAAGACTG	GGGTAAATAC	420
ATTAAATCCA	CAGGATGAAG	TTTTATCAGG	TCAATTGAAC	AAACCTGAAC	TCTTATATCG	480
TGAGGAAACT	ATGGAGACAA	AAATAGATTT	TCAAGAAGAA	ATTCAAGAAA	ATCCTGATTT	540
AGCTGAAGGA	ACTGTAAGAG	TAAACAAGA	AGGTAAATTA	GGTAAGAAAG	TTGAAATCGT	600
CAGAATATTC	TCTGTAAACA	AGGAAGAAGT	TTCGCGAGAA	ATTGTTTCAA	CTTCAACGAC	660
TGCGCCTAGT	CCAAGAATAG	TCGAAAAAGG	TACTAAAAAA	ACTCAAGTTA	TAAAGGAACA	720
ACCTGAGACT	GGTGTAGAAC	ATAAGGACGT	ACAGTCTGGA	GCTATTGTTG	AACCCGCAAT	780
TCAGCCTGAG	TTGCCCGAAG	CTGTAGTAAG	TGACAAAGGC	GAACCAGAAG	TTCAACCTAC	840

ATTACCCGAA GCAGTTGTGA CCGACAAAGG TGAGACTGAG GTTCAACCAG AGTCGCCAGA 900  
TACTGTGGTA ACTGATAAAG GTGAACCAGA GCAGGTAGCA CCGCTTCCAG AATATAAGGG 960  
TAATATTGAG CAAGTAAAC CTGAAACTCC GGTGAGAAG ACCAAAGAAC AAGGTCCAGA 1020  
AAAAACTGAA GAAGTTCCAG TAAACCAAC AGAAGAAACA CCAGTAAATC CAAATGAAGG 1080  
TACTACAGAA GGAACCTCAA TTCAAGAAGC AGAAAATCCA GTTCAACCTG CAGAAGAATC 1140  
AACACGAAT TCAGAGAAAG TATCACCAGA TACATCTAGC AAAAATACTG GGAAGTGTC 1200  
CAGTAATCCT AGTGATTCGA CAACCTCAGT TGGAGAATCA AATAAACAG AACATAATGA 1260  
CTCTAAAAAT GAAAATTCAG AAAAACTGT AGAAGAAGTT CCAGTAAATC CAAATGAAGG 1320  
CACAGTAGAA GGTACCTCAA ATCAAGAAAC AGAAAAACCA GTTCAACCTG CAGAAGAAAC 1380  
ACAAACAAAC TCTGGGAAAA TAGCTAACGA AAATACTGGA GAAGTATCCA ATAAACCTAG 1440  
TGATTCAAAA CCACCAGTTG AAGAATCAAA TCAACCAGAA AAAAACGGAA CTGCAACAAA 1500  
ACCAGAAAAT TCAGGTAATA CAACATCAGA GAATGGACAA ACAGAACCAG AACCATCAAA 1560  
CGGAAATTCA ACTGAGGATG TTTCAACCGA ATCAAACACA TCCAATTCAA ATGGAAACGA 1620  
AGAAATTAAA CAAGAAAATG AACTAGACCC TGATAAAAAG GTAGAAGAAC CAGAGAAAAC 1680  
ACTTGAATTA AGAAATGTTT CCGACCTAGA GTTA 1714

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asn Tyr Asn Thr Asp Tyr Glu Leu Thr Ser Gly Glu Lys Leu Pro Leu  
1 5 10 15  
Pro Lys Glu Ile Ser Gly Tyr Thr Tyr Ile Gly Tyr Ile Lys Glu Gly  
20 25 30  
Lys Thr Thr Ser Glu Ser Glu Val Ser Asn Gln Lys Ser Ser Val Ala  
35 40 45  
Thr Pro Thr Lys Gln Gln Lys Val Asp Tyr Asn Val Thr Pro Asn Phe  
50 55 60  
Val Asp His Pro Ser Thr Val Gln Ala Ile Gln Glu Gln Thr Pro Val  
65 70 75 80  
Ser Ser Thr Lys Pro Thr Glu Val Gln Val Val Glu Lys Pro Phe Ser  
85 90 95  
Thr Glu Leu Ile Asn Pro Arg Lys Glu Glu Lys Gln Ser Ser Asp Ser  
100 105 110

0965272.012201

Gln Glu Gln Leu Ala Glu His Lys Asn Leu Glu Thr Lys Lys Glu Glu  
 115 120 125  
 Lys Ile Ser Pro Lys Glu Lys Thr Gly Val Asn Thr Leu Asn Pro Gln  
 130 135 140  
 Asp Glu Val Leu Ser Gly Gln Leu Asn Lys Pro Glu Leu Leu Tyr Arg  
 145 150 155 160  
 Glu Glu Thr Met Glu Thr Lys Ile Asp Phe Gln Glu Glu Ile Gln Glu  
 165 170 175  
 Asn Pro Asp Leu Ala Glu Gly Thr Val Arg Val Lys Gln Glu Gly Lys  
 180 185 190  
 Leu Gly Lys Lys Val Glu Ile Val Arg Ile Phe Ser Val Asn Lys Glu  
 195 200 205  
 Glu Val Ser Arg Glu Ile Val Ser Thr Ser Thr Thr Ala Pro Ser Pro  
 210 215 220  
 Arg Ile Val Glu Lys Gly Thr Lys Lys Thr Gln Val Ile Lys Glu Gln  
 225 230 235 240  
 Pro Glu Thr Gly Val Glu His Lys Asp Val Gln Ser Gly Ala Ile Val  
 245 250 255  
 Glu Pro Ala Ile Gln Pro Glu Leu Pro Glu Ala Val Val Ser Asp Lys  
 260 265 270  
 Gly Glu Pro Glu Val Gln Pro Thr Leu Pro Glu Ala Val Val Thr Asp  
 275 280 285  
 Lys Gly Glu Thr Glu Val Gln Pro Glu Ser Pro Asp Thr Val Val Ser  
 290 295 300  
 Asp Lys Gly Glu Pro Glu Gln Val Ala Pro Leu Pro Glu Tyr Lys Gly  
 305 310 315 320  
 Asn Ile Glu Gln Val Lys Pro Glu Thr Pro Val Glu Lys Thr Lys Glu  
 325 330 335  
 Gln Gly Pro Glu Lys Thr Glu Glu Val Pro Val Lys Pro Thr Glu Glu  
 340 345 350  
 Thr Pro Val Asn Pro Asn Glu Gly Thr Thr Glu Gly Thr Ser Ile Gln  
 355 360 365  
 Glu Ala Glu Asn Pro Val Gln Pro Ala Glu Glu Ser Thr Thr Asn Ser  
 370 375 380  
 Glu Lys Val Ser Pro Asp Thr Ser Ser Lys Asn Thr Gly Glu Val Ser  
 385 390 395 400  
 Ser Asn Pro Ser Asp Ser Thr Thr Ser Val Gly Glu Ser Asn Lys Pro  
 405 410 415  
 Glu His Asn Asp Ser Lys Asn Glu Asn Ser Glu Lys Thr Val Glu Glu  
 420 425 430  
 Val Pro Val Asn Pro Asn Glu Gly Thr Val Glu Gly Thr Ser Asn Gln  
 435 440 445

09765272 012201

Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn Ser  
450 455 460

Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro Ser  
465 470 475 480

Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn Gly  
485 490 495

Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn Gly  
500 505 510

Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val Ser  
515 520 525

Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys Gln  
530 535 540

Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys Thr  
545 550 555 560

Leu Glu Leu Arg Asn Val Ser Asp Leu Glu Leu  
565 570

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGAGAATCAA GCTACACCCA AAGAGACTAG CGCTCAAAAG ACAATCGTCC TTGCTACAGC	60
TGGCGACGTG CCACCATTTG ACTACGAAGA CAAGGGCAAT CTGACAGGCT TTGATATCGA	120
AGTTTTAAAG GCAGTAGATG AAAAAGCTCAG CGACTACGAG ATTCAATTCC AAAGAACCGC	180
CTGGGAGAGC ATCTTCCAG GACTTGATTC TGGTCACTAT CAGGCTGCGG CCAATAACTT	240
GAGTTACACA AAAGAGCGTG CTGAAAAATA CCTTTACTCG CTTCCAATTT CCAACAATCC	300
CCTCGTCCTT GTCAGCAACA AGAAAAATCC TTTGACTTCT CTTGACCAGA TCGCTGGTAA	360
AACAACACAA GAGGATACCG GAACTTCTAA CGCTCAATTC ATCAATAACT GGAATCAGAA	420
ACACACTGAT AATCCCGCTA CAATTAATTT TTCTGGTGAG GATATTGGTA AACGAATCCT	480
AGACCTTGCT AACGGAGAGT TTGATTTCT AGTTTTTGAC AAGGTATCCG TTCAAAAGAT	540
TATCAAGGAC CGTGGTTTAG ACCTCTCAGT CGTTGATTTA CCTTCTGCAG ATAGCCCCAG	600
CAATTATATC ATTTTCTCAA GCGACCAAAA AGAGTTTAAA GAGCAATTTG ATAAAGCGCT	660
CAAAGAACTC TATCAAGACG GAACCCTTGA AAAACTCAGC AATACCTATC TAGGTGGTTC	720
TTACCTCCCA GATCAATCTC AGTTACAA	748

09765272.012201

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Asn Gln Ala Thr Pro Lys Glu Thr Ser Ala Gln Lys Thr Ile Val  
 1 5 10 15  
 Leu Ala Thr Ala Gly Asp Val Pro Pro Phe Asp Tyr Glu Asp Lys Gly  
 20 25 30  
 Asn Leu Thr Gly Phe Asp Ile Glu Val Leu Lys Ala Val Asp Glu Lys  
 35 40 45  
 Leu Ser Asp Tyr Glu Ile Gln Phe Gln Arg Thr Ala Trp Glu Ser Ile  
 50 55 60  
 Phe Pro Gly Leu Asp Ser Gly His Tyr Gln Ala Ala Ala Asn Asn Leu  
 65 70 75 80  
 Ser Tyr Thr Lys Glu Arg Ala Glu Lys Tyr Leu Tyr Ser Leu Pro Ile  
 85 90 95  
 Ser Asn Asn Pro Leu Val Leu Val Ser Asn Lys Lys Asn Pro Leu Thr  
 100 105 110  
 Ser Leu Asp Gln Ile Ala Gly Lys Thr Thr Gln Glu Asp Thr Gly Thr  
 115 120 125  
 Ser Asn Ala Gln Phe Ile Asn Asn Trp Asn Gln Lys His Thr Asp Asn  
 130 135 140  
 Pro Ala Thr Ile Asn Phe Ser Gly Glu Asp Ile Gly Lys Arg Ile Leu  
 145 150 155 160  
 Asp Leu Ala Asn Gly Glu Phe Asp Phe Leu Val Phe Asp Lys Val Ser  
 165 170 175  
 Val Gln Lys Ile Ile Lys Asp Arg Gly Leu Asp Leu Ser Val Val Asp  
 180 185 190  
 Leu Pro Ser Ala Asp Ser Pro Ser Asn Tyr Ile Ile Phe Ser Ser Asp  
 195 200 205  
 Gln Lys Glu Phe Lys Glu Gln Phe Asp Lys Ala Leu Lys Glu Leu Tyr  
 210 215 220  
 Gln Asp Gly Thr Leu Glu Lys Leu Ser Asn Thr Tyr Leu Gly Gly Ser  
 225 230 235 240  
 Tyr Leu Pro Asp Gln Ser Gln Leu Gln  
 245

## (2) INFORMATION FOR SEQ ID NO: 7:

09765272.012201

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGGTAACCGC TCTTCTCGTA ACGCAGCTTC ATCTTCTGAT GTGAAGACAA AAGCAGCAAT 60  
 CGTCACTGAT ACTGGTGGTG TTGATGACAA ATCATTCAAC CAATCAGCTT GGGAAGGTTT 120  
 GCAGGCTTGG GGTAAAGAAC ACAATCTTTC AAAAGATAAC GGTTTCACTT ACTTCCAATC 180  
 AACAAGTGAA GCTGACTACG CTAACAACCTT GCAACAAGCG GCTGGAAGTT ACAACCTAAT 240  
 CTCGGTGTGTT GGTTTTGCCC TTAATAATGC AGTTAAAGAT GCAGCAAAAG AACACACTGA 300  
 CTTGAACTAT GTCTTGATTG ATGATGTGAT TAAAGACCAA AAGAATGTTG CGAGCGTAAC 360  
 TTTGCTGAT AATGAGTCAG GTTACCTTGC AGGTGTGGCT GCAGCAAAAA CAACTAAGAC 420  
 AAAACAAGTT GGTTTTGTAG GTGGTATCGA ATCTGAAGTT ATCTCTCGTT TTGAAGCAGG 480  
 ATTCAAGGCT GGTGTTGCGT CAGTAGACCC ATCTATCAAA GTCCAAGTTG ACTACGCTGG 540  
 TTCATTGGT GATGCGGCTA AAGGTAAAAC AATTGCAGCC GCACAATACG CAGCCGGTGC 600  
 AGATATTGTT TACCAAGTAG CTGGTGGTAC AGGTGCAGGT GTCTTTGCAG AGGCAAAATC 660  
 TCTCAACGAA AGCCGTCCTG AAAATGAAAA AGTTTGGGTT ATCGGTGTTG ATCGTGACCA 720  
 AGAAGCAGAA GGTAATACA CTTCTAAAGA TGGCAAAGAA TCAAACCTTG TTCTTGATC 780  
 TACTTTGAAA CAAGTTGGTA CAACTGTAAA AGATATTTCT AACAAGGCAG AAAGAGGAGA 840  
 ATTCCCTGGC GGTCAAGTGA TCGTTTACTC ATTGAAGGAT AAAGGGGTTG ACTTGGCAGT 900  
 AACAAACCTT TCAGAAGAAG GTAAAAAAGC TGTCGAAGAT GCAAAAGCTA AAATCCTTGA 960  
 TGGAAGCGTA AAAGTTCCTG AAAAA 985

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser Ser Ser Asp Val Lys Thr  
 1 5 10 15

Lys Ala Ala Ile Val Thr Asp Thr Gly Gly Val Asp Asp Lys Ser Phe  
 20 25 30

Asn Gln Ser Ala Trp Glu Gly Leu Gln Ala Trp Gly Lys Glu His Asn

09765272.012201

35

40

45

Leu Ser Lys Asp Asn Gly Phe Thr Tyr Phe Gln Ser Thr Ser Glu Ala  
 50 55 60  
 Asp Tyr Ala Asn Asn Leu Gln Gln Ala Ala Gly Ser Tyr Asn Leu Ile  
 65 70 75 80  
 Phe Gly Val Gly Phe Ala Leu Asn Asn Ala Val Lys Asp Ala Ala Lys  
 85 90 95  
 Glu His Thr Asp Leu Asn Tyr Val Leu Ile Asp Asp Val Ile Lys Asp  
 100 105 110  
 Gln Lys Asn Val Ala Ser Val Thr Phe Ala Asp Asn Glu Ser Gly Tyr  
 115 120 125  
 Leu Ala Gly Val Ala Ala Ala Lys Thr Thr Lys Thr Lys Gln Val Gly  
 130 135 140  
 Phe Val Gly Gly Ile Glu Ser Glu Val Ile Ser Arg Phe Glu Ala Gly  
 145 150 155 160  
 Phe Lys Ala Gly Val Ala Ser Val Asp Pro Ser Ile Lys Val Gln Val  
 165 170 175  
 Asp Tyr Ala Gly Ser Phe Gly Asp Ala Ala Lys Gly Lys Thr Ile Ala  
 180 185 190  
 Ala Ala Gln Tyr Ala Ala Gly Ala Asp Ile Val Tyr Gln Val Ala Gly  
 195 200 205  
 Gly Thr Gly Ala Gly Val Phe Ala Glu Ala Lys Ser Leu Asn Glu Ser  
 210 215 220  
 Arg Pro Glu Asn Glu Lys Val Trp Val Ile Gly Val Asp Arg Asp Gln  
 225 230 235 240  
 Glu Ala Glu Gly Lys Tyr Thr Ser Lys Asp Gly Lys Glu Ser Asn Phe  
 245 250 255  
 Val Leu Val Ser Thr Leu Lys Gln Val Gly Thr Thr Val Lys Asp Ile  
 260 265 270  
 Ser Asn Lys Ala Glu Arg Gly Glu Phe Pro Gly Gly Gln Val Ile Val  
 275 280 285  
 Tyr Ser Leu Lys Asp Lys Gly Val Asp Leu Ala Val Thr Asn Leu Ser  
 290 295 300  
 Glu Glu Gly Lys Lys Ala Val Glu Asp Ala Lys Ala Lys Ile Leu Asp  
 305 310 315 320  
 Gly Ser Val Lys Val Pro Glu Lys  
 325

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

09765272.012201



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGCTGATT CAGGTGACAA ACCTGTTATC	60
AAAATGTACC AAATCGGTGA CAAACCAGAC AACTTGGATG AATTGTTAGC AAATGCCAAC	120
AAAATCATTG AAGAAAAAGT TGGTGCCAAA TTGGATATCC AATACCTTGG CTGGGGGTGAC	180
TATGGTAAGA AAATGTCAGT TATCACATCA TCTGGTGAAA ACTATGATAT TGCCTTTGCA	240
GATAACTATA TTGTAAATGC TCAAAAAGGT GCTTACGCTG ACTTGACAGA ATTGTACAAA	300
AAAGAAGGTA AAGACCTTTA CAAAGCACTT GACCCAGCTT ACATCAAGGG TAATACTGTA	360
AATGGTAAGA TTTACGCTGT TCCAGTTGCA GCCAACGTTG CATCATCTCA AAACCTTGCC	420
TTCAACGGAA CTCTCCTTGC TAAATATGGT ATCGATATTT CAGGTGTTAC TTCTTACGAA	480
ACTCTTGAGC CAGTCTTGAA ACAAAATCAAA GAAAAAGCTC CAGACGTAGT ACCATTTGCT	540
ATTGGTAAAG TTTTCATCCC ATCTGATAAT TTTGACTACC CAGTAGCAAA CGGTCTTCCA	600
TTCGTTATCG ACCTTGAAGG CGATACTACT AAAGTTGTAA ACCGTTACGA AGTGCCTCGT	660
TTCAAAGAAC ACTTGAAGAC TCTTCACAAA TTCTATGAAG CTGGCTACAT TCCAAAAGAC	720
GTCGCAACAA GCGATACTTC CTTTGACCTT CAACAAGATA CTTGGTTCGT TCGTGAAGAA	780
ACAGTAGGAC CAGCTGACTA CGGTAACAGC TTGCTTTCAC GTGTTGCCAA CAAAGATATC	840
CAAATCAAAC CAATTACTAA CTTTCATCAAG NAAAACCAAA CAACACAAGT TGCTAACTTT	900
GTCATCTCAA ACAACTCTAA GAACAAAGAA AAATCAATGG AAATCTTGAA CCTCTTGAAT	960
ACGAACCCAG AACTCTTGAA CGGTCTTGTT TACGGTCCAG AAGGCAAGAA CTGGGAAAAA	1020
ATTGAAGGTA AAGAAAACCG TGTTGCGGTT CTTGATGGCT ACAAAGGAAA CACTCACATG	1080
GGTGGATGGA ACACTGGTAA CAACTGGATC CTTTACATCA ACGAAAACGT TACAGACCAA	1140
CAAATCGAAA ATTCTAAGAA AGAATTGGCA GAAGCTAAAG AATCTCCAGC GCTTGGATTT	1200
ATCTTCAATA CTGACAATGT GAAATCTGAA ATCTCAGCTA TTGCTAACAC AATGCAACAA	1260
TTTGATACAG CTATCAACAC TGGTACTGTA GACCCAGATA AAGCGATTCC AGAATTGATG	1320
GAAAAATTGA AATCTGAAGG TGCCTACGAA AAAGTATTGA ACGAAATGCA AAAACAATAC	1380
GATGAATTCT TGAAAAACAA AAAA	1404

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

09765272.012204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Gly Asn Leu Thr Gly Asn Ser Lys Lys Ala Ala Asp Ser Gly Asp  
 1 5 10 15  
 Lys Pro Val Ile Lys Met Tyr Gln Ile Gly Asp Lys Pro Asp Asn Leu  
 20 25 30  
 Asp Glu Leu Leu Ala Asn Ala Asn Lys Ile Ile Glu Glu Lys Val Gly  
 35 40 45  
 Ala Lys Leu Asp Ile Gln Tyr Leu Gly Trp Gly Asp Tyr Gly Lys Lys  
 50 55 60  
 Met Ser Val Ile Thr Ser Ser Gly Glu Asn Tyr Asp Ile Ala Phe Ala  
 65 70 75 80  
 Asp Asn Tyr Ile Val Asn Ala Gln Lys Gly Ala Tyr Ala Asp Leu Thr  
 85 90 95  
 Glu Leu Tyr Lys Lys Glu Gly Lys Asp Leu Tyr Lys Ala Leu Asp Pro  
 100 105 110  
 Ala Tyr Ile Lys Gly Asn Thr Val Asn Gly Lys Ile Tyr Ala Val Pro  
 115 120 125  
 Val Ala Ala Asn Val Ala Ser Ser Gln Asn Phe Ala Phe Asn Gly Thr  
 130 135 140  
 Leu Leu Ala Lys Tyr Gly Ile Asp Ile Ser Gly Val Thr Ser Tyr Glu  
 145 150 155 160  
 Thr Leu Glu Pro Val Leu Lys Gln Ile Lys Glu Lys Ala Pro Asp Val  
 165 170 175  
 Val Pro Phe Ala Ile Gly Lys Val Phe Ile Pro Ser Asp Asn Phe Asp  
 180 185 190  
 Tyr Pro Val Ala Asn Gly Leu Pro Phe Val Ile Asp Leu Glu Gly Asp  
 195 200 205  
 Thr Thr Lys Val Val Asn Arg Tyr Glu Val Pro Arg Phe Lys Glu His  
 210 215 220  
 Leu Lys Thr Leu His Lys Phe Tyr Glu Ala Gly Tyr Ile Pro Lys Asp  
 225 230 235 240  
 Val Ala Thr Ser Asp Thr Ser Phe Asp Leu Gln Gln Asp Thr Trp Phe  
 245 250 255  
 Val Arg Glu Glu Thr Val Gly Pro Ala Asp Tyr Gly Asn Ser Leu Leu  
 260 265 270  
 Ser Arg Val Ala Asn Lys Asp Ile Gln Ile Lys Pro Ile Thr Asn Phe  
 275 280 285  
 Ile Lys Xaa Asn Gln Thr Thr Gln Val Ala Asn Phe Val Ile Ser Asn  
 290 295 300  
 Asn Ser Lys Asn Lys Glu Lys Ser Met Glu Ile Leu Asn Leu Leu Asn  
 305 310 315 320  
 Thr Asn Pro Glu Leu Leu Asn Gly Leu Val Tyr Gly Pro Glu Gly Lys

09765272.012201

325

330

335

Asn Trp Glu Lys Ile Glu Gly Lys Glu Asn Arg Val Arg Val Leu Asp  
340 345 350

Gly Tyr Lys Gly Asn Thr His Met Gly Gly Trp Asn Thr Gly Asn Asn  
355 360 365

Trp Ile Leu Tyr Ile Asn Glu Asn Val Thr Asp Gln Gln Ile Glu Asn  
370 375 380

Ser Lys Lys Glu Leu Ala Glu Ala Lys Glu Ser Pro Ala Leu Gly Phe  
385 390 395 400

Ile Phe Asn Thr Asp Asn Val Lys Ser Glu Ile Ser Ala Ile Ala Asn  
405 410 415

Thr Met Gln Gln Phe Asp Thr Ala Ile Asn Thr Gly Thr Val Asp Pro  
420 425 430

Asp Lys Ala Ile Pro Glu Leu Met Glu Lys Leu Lys Ser Glu Gly Ala  
435 440 445

Tyr Glu Lys Val Leu Asn Glu Met Gln Lys Gln Tyr Asp Glu Phe Leu  
450 455 460

Lys Asn Lys Lys  
465

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGGTCAAGGA ACTGCTTCTA AAGACAACAA AGAGGCAGAA CTTAAGAAGG TTGACTTTAT	60
CCTAGACTGG ACACCAAATA CCAACCACAC AGGGCTTTAT GTTGCCAAGG AAAAAGGTTA	120
TTTCAAAGAA GCTGGAGTGG ATGTTGATTT GAAATTGCCA CCAGAAGAAA GTTCTTCTGA	180
CTTGTTATC AACGGAAAGG CACCATTTGC AGTGTATTTT CAAGACTACA TGGCTAAGAA	240
ATTGGAAAAA GGAGCAGGAA TCACTGCCGT TGCAGCTATT GTTGAACACA ATACATCAGG	300
AATCATCTCT CGTAAATCTG ATAATGTAAG CAGTCCAAAA GACTTGTTG GTAAGAAATA	360
TGGGACATGG AATGACCCAA CTGAACTTGC TATGTTGAAA ACCTTGGTAG AATCTCAAGG	420
TGGAGACTTT GAGAAGGTTG AAAAAGTACC AAATAACGAC TCAAACCTCA TCACACCGAT	480
TGCCAATGGC GTCTTTGATA CTGCTTGGAT TTACTACGGT TGGGATGGTA TCCTTGCTAA	540
ATCTCAAGGT GTAGATGCTA ACTTCATGTA CTTGAAAGAC TATGTCAAGG AGTTTGACTA	600
CTATTCACCA GTTATCATCG CAAACAACGA CTATCTGAAA GATAACAAAG AAGAAGCTCG	660
CAAAGTCATC CAAGCCATCA AAAAAGGCTA CCAATATGCC ATGGAACATC CAGAAGAAGC	720

09765272.012201

TGCAGATATT CTCATCAAGA ATGCACCTGA ACTCAAGGAA AAACGTGACT TTGTCATCGA 780  
 ATCTCAAAAA TACTTGTCAA AAGAATACGC AAGCGACAAG GAAAAATGGG GTCAATTTGA 840  
 CGCAGCTCGC TGAATGCTT TCTACAAATG GGATAAAGAA AATGGTATCC TTAAAGAAGA 900  
 CTTGACAGAC AAAGGCTTCA CCAACGAATT TGTGAAA 937

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Gln Gly Thr Ala Ser Lys Asp Asn Lys Glu Ala Glu Leu Lys Lys  
 1 5 10 15  
 Val Asp Phe Ile Leu Asp Trp Thr Pro Asn Thr Asn His Thr Gly Leu  
 20 25 30  
 Tyr Val Ala Lys Glu Lys Gly Tyr Phe Lys Glu Ala Gly Val Asp Val  
 35 40 45  
 Asp Leu Lys Leu Pro Pro Glu Glu Ser Ser Ser Asp Leu Val Ile Asn  
 50 55 60  
 Gly Lys Ala Pro Phe Ala Val Tyr Phe Gln Asp Tyr Met Ala Lys Lys  
 65 70 75 80  
 Leu Glu Lys Gly Ala Gly Ile Thr Ala Val Ala Ala Ile Val Glu His  
 85 90 95  
 Asn Thr Ser Gly Ile Ile Ser Arg Lys Ser Asp Asn Val Ser Ser Pro  
 100 105 110  
 Lys Asp Leu Val Gly Lys Lys Tyr Gly Thr Trp Asn Asp Pro Thr Glu  
 115 120 125  
 Leu Ala Met Leu Lys Thr Leu Val Glu Ser Gln Gly Gly Asp Phe Glu  
 130 135 140  
 Lys Val Glu Lys Val Pro Asn Asn Asp Ser Asn Ser Ile Thr Pro Ile  
 145 150 155 160  
 Ala Asn Gly Val Phe Asp Thr Ala Trp Ile Tyr Tyr Gly Trp Asp Gly  
 165 170 175  
 Ile Leu Ala Lys Ser Gln Gly Val Asp Ala Asn Phe Met Tyr Leu Lys  
 180 185 190  
 Asp Tyr Val Lys Glu Phe Asp Tyr Tyr Ser Pro Val Ile Ile Ala Asn  
 195 200 205  
 Asn Asp Tyr Leu Lys Asp Asn Lys Glu Glu Ala Arg Lys Val Ile Gln  
 210 215 220

09765272.012201

Ala Ile Lys Lys Gly Tyr Gln Tyr Ala Met Glu His Pro Glu Glu Ala  
 225 230 235 240

Ala Asp Ile Leu Ile Lys Asn Ala Pro Glu Leu Lys Glu Lys Arg Asp  
 245 250 255

Phe Val Ile Glu Ser Gln Lys Tyr Leu Ser Lys Glu Tyr Ala Ser Asp  
 260 265 270

Lys Glu Lys Trp Gly Gln Phe Asp Ala Ala Arg Trp Asn Ala Phe Tyr  
 275 280 285

Lys Trp Asp Lys Glu Asn Gly Ile Leu Lys Glu Asp Leu Thr Asp Lys  
 290 295 300

Gly Phe Thr Asn Glu Phe Val Lys  
 305 310

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAGCTCAGGT GGAAACGCTG GTTCATCCTC TGGAAAAACA ACTGCCAAAG CTCGCACTAT	60
CGATGAAATC AAAAAAGCG GTGAAGTGGC AATCGCCGTG TTTGGAGATA AAAAACCGTT	120
TGGCTACGTT GACAATGATG GTTCTACCAA GGTACGCTAC GATATTGAAC TAGGGAACCA	180
ACTAGCTCAA GACCTTGGTG TCAAGGTAA ATACATTTCG GTCGATGCTG CCAACCGTGC	240
GGAATACTTG ATTTCAAACA AGGTAGATAT TACTCTTGCT AACTTTACAG TAACTGACGA	300
ACGTAAGAAA CAAGTTGATT TTGCCCTTCC ATATATGAAA GTTTCTCTGG GTGTCGTATC	360
ACCTAAGACT GGTCTCATT CAGACGTCAA ACAACTTGAA GGTAACCT TAATTGTCAC	420
AAAAGGA 3 ACTGCTGAGA CTTATTTTGA AAAGAATCAT CCAGAAATCA AACTCCAAAA	480
ATACGACCAA TACAGTGAAT CTTACCAAGC TCTTCTTGAC GGACGTGGAG ATGCCTTTTC	540
AACTGACAAT ACGGAAGTTC TAGCTTGGGC GCTTGAAAAT AAAGGATTTG AAGTAGGAAT	600
TACTTCCCTC GGTGATCCCG ATACCATTGC GGCAGCAGTT CAAAAGGCA ACCAAGAATT	660
GCTAGACTTC ATCAATAAAG ATATTGAAAA ATTAGGCAAG GAAACTTCT TCCACAAGGC	720
CTATGAAAAG ACACTTCACC CAACCTACGG TGACGCTGCT AAAGCAGATG ACCTGGTTGT	780
TGAAGGTGGA AAAGTTGAT	799

## (2) INFORMATION FOR SEQ ID NO: 14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid

09765272.012201

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser	Ser	Gly	Gly	Asn	Ala	Gly	Ser	Ser	Ser	Gly	Lys	Thr	Thr	Ala	Lys	1	5	10	15
Ala	Arg	Thr	Ile	Asp	Glu	Ile	Lys	Lys	Ser	Gly	Glu	Leu	Arg	Ile	Ala	20	25	30	
Val	Phe	Gly	Asp	Lys	Lys	Pro	Phe	Gly	Tyr	Val	Asp	Asn	Asp	Gly	Ser	35	40	45	
Thr	Lys	Val	Arg	Tyr	Asp	Ile	Glu	Leu	Gly	Asn	Gln	Leu	Ala	Gln	Asp	50	55	60	
Leu	Gly	Val	Lys	Val	Lys	Tyr	Ile	Ser	Val	Asp	Ala	Ala	Asn	Arg	Ala	65	70	75	80
Glu	Tyr	Leu	Ile	Ser	Asn	Lys	Val	Asp	Ile	Thr	Leu	Ala	Asn	Phe	Thr	85	90	95	
Val	Thr	Asp	Glu	Arg	Lys	Lys	Gln	Val	Asp	Phe	Ala	Leu	Pro	Tyr	Met	100	105	110	
Lys	Val	Ser	Leu	Gly	Val	Val	Ser	Pro	Lys	Thr	Gly	Leu	Ile	Thr	Asp	115	120	125	
Val	Lys	Gln	Leu	Glu	Gly	Lys	Thr	Leu	Ile	Val	Thr	Lys	Gly	Thr	Thr	130	135	140	
Ala	Glu	Thr	Tyr	Phe	Glu	Lys	Asn	His	Pro	Glu	Ile	Lys	Leu	Gln	Lys	145	150	155	160
Tyr	Asp	Gln	Tyr	Ser	Asp	Ser	Tyr	Gln	Ala	Leu	Leu	Asp	Gly	Arg	Gly	165	170	175	
Asp	Ala	Phe	Ser	Thr	Asp	Asn	Thr	Glu	Val	Leu	Ala	Trp	Ala	Leu	Glu	180	185	190	
Asn	Lys	Gly	Phe	Glu	Val	Gly	Ile	Thr	Ser	Leu	Gly	Asp	Pro	Asp	Thr	195	200	205	
Ile	Ala	Ala	Ala	Val	Gln	Lys	Gly	Asn	Gln	Glu	Leu	Leu	Asp	Phe	Ile	210	215	220	
Asn	Lys	Asp	Ile	Glu	Lys	Leu	Gly	Lys	Glu	Asn	Phe	Phe	His	Lys	Ala	225	230	235	240
Tyr	Glu	Lys	Thr	Leu	His	Pro	Thr	Tyr	Gly	Asp	Ala	Ala	Lys	Ala	Asp	245	250	255	
Asp	Leu	Val	Val	Glu	Gly	Gly	Lys	Val	Asp							260	265		

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1189 base pairs

09765272.012201

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCCAAC	TAT	GGTAAATCTG	CGGATGGCAC	AGTGACCATC	GAGTATTTCA	ACCAGAAAAA	60
AGAAATGACC	AAAACCTTGG	AAGAAATCAC	TCGTGATTTT	GAGAAGGAAA	ACCCTAAGAT		120
CAAGGTCAAA	GTCGTCAATG	TACCAAATGC	TGGTGAAGTA	TTGAAGACAC	GCGTTCTCGC		180
AGGAGATGTG	CCTGATGTGG	TCAATATTTA	CCCACAGTCC	ATCGAACTGC	AAGAATGGGC		240
AAAAGCAGGT	GTTTTTGAAG	ATTTGAGCAA	CAAAGACTAC	CTGAAACGCG	TGAAAAATGG		300
CTACGCTGAA	AAATATGCTG	TAAACGAAAA	AGTTTACAAC	GTTCTTTTTA	CAGCTAATGC		360
TTATGGAATT	TACTACAACA	AAGATAAATT	CGAAGAAGT	GGCTTGAAGG	TTCCTGAAAC		420
CTGGGATGAA	TTTGAACAGT	TAGTCAAAGA	TATCGTTGCT	AAAGGACAAA	CACCATTG		480
AATTGCAGGT	GCAGATGCTT	GGACACTCAA	TGGTTACAAT	CAATTAGCCT	TTGCGACAGC		540
AACAGGTGGA	GGAAAAGAAG	CAAATCAATA	CCTTCGTTAT	TCTCAACCAA	ATGCCATTAA		600
ATTGTCGGAT	CCGATTATGA	AAGATGATAT	CAAGGTCATG	GACATCCTTC	GCATCAATGG		660
ATCTAAGCAA	AAGAACTGGG	AAGGTGCTGG	CTATACCGAT	GTTATCGGAG	CCTTCGCACG		720
TGGGGATGTC	CTCATGACAC	CAAATGGGTC	TTGGGCGATC	ACAGCGATTA	ATGAACAAAA		780
ACCGAACTTT	AAGATTGGGA	CCTTCATGAT	TCCAGGAAAA	GAAAAAGGAC	AAAGCTTAAC		840
CGTTGGTGCG	GGAGACTTGG	CATGGTCTAT	CTCAGCCACC	ACCAAACATC	CAAAAGAAGC		900
CAATGCCTTT	GTGGAATATA	TGACCCGTCC	AGAAGTCATG	CAAAAATACT	ACGATGTGGA		960
CGGATCTCCA	ACAGCGATCG	AAGGGGTCAA	ACAAGCAGGA	GAAGATTAC	CGCTTGCTGG		1020
TATGACCGAA	TATGCCTTTA	CGGATCGTCA	CTTGGTCTGG	TTGCAACAAT	ACTGGACCAG		1080
TGAAGCAGAC	TTCCATACCT	TGACCATGAA	CTATGTCTTG	ACCGGTGATA	AACAAGGCAT		1140
GGTCAATGAT	TTGAATGCCT	TCTTTAACCC	GATGAAAGCG	GATGTGGAT			1189

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser	Asn	Tyr	Gly	Lys	Ser	Ala	Asp	Gly	Thr	Val	Thr	Ile	Glu	Tyr	Phe
1				5				10						15	

09765272-012201

Asn	Gln	Lys	Lys	Glu	Met	Thr	Lys	Thr	Leu	Glu	Glu	Ile	Thr	Arg	Asp	
			20					25					30			
Phe	Glu	Lys	Glu	Asn	Pro	Lys	Ile	Lys	Val	Lys	Val	Val	Asn	Val	Pro	
		35					40					45				
Asn	Ala	Gly	Glu	Val	Leu	Lys	Thr	Arg	Val	Leu	Ala	Gly	Asp	Val	Pro	
	50					55					60					
Asp	Val	Val	Asn	Ile	Tyr	Pro	Gln	Ser	Ile	Glu	Leu	Gln	Glu	Trp	Ala	
65					70					75					80	
Lys	Ala	Gly	Val	Phe	Glu	Asp	Leu	Ser	Asn	Lys	Asp	Tyr	Leu	Lys	Arg	
				85					90					95		
Val	Lys	Asn	Gly	Tyr	Ala	Glu	Lys	Tyr	Ala	Val	Asn	Glu	Lys	Val	Tyr	
			100					105					110			
Asn	Val	Pro	Phe	Thr	Ala	Asn	Ala	Tyr	Gly	Ile	Tyr	Tyr	Asn	Lys	Asp	
		115					120					125				
Lys	Phe	Glu	Glu	Leu	Gly	Leu	Lys	Val	Pro	Glu	Thr	Trp	Asp	Glu	Phe	
	130					135					140					
Glu	Gln	Leu	Val	Lys	Asp	Ile	Val	Ala	Lys	Gly	Gln	Thr	Pro	Phe	Gly	
145					150					155					160	
Ile	Ala	Gly	Ala	Asp	Ala	Trp	Thr	Leu	Asn	Gly	Tyr	Asn	Gln	Leu	Ala	
				165					170					175		
Phe	Ala	Thr	Ala	Thr	Gly	Gly	Gly	Lys	Glu	Ala	Asn	Gln	Tyr	Leu	Arg	
			180					185					190			
Tyr	Ser	Gln	Pro	Asn	Ala	Ile	Lys	Leu	Ser	Asp	Pro	Ile	Met	Lys	Asp	
		195					200					205				
Asp	Ile	Lys	Val	Met	Asp	Ile	Leu	Arg	Ile	Asn	Gly	Ser	Lys	Gln	Lys	
	210					215					220					
Asn	Trp	Glu	Gly	Ala	Gly	Tyr	Thr	Asp	Val	Ile	Gly	Ala	Phe	Ala	Arg	
225					230					235					240	
Gly	Asp	Val	Leu	Met	Thr	Pro	Asn	Gly	Ser	Trp	Ala	Ile	Thr	Ala	Ile	
				245					250				255			
Asn	Glu	Gln	Lys	Pro	Asn	Phe	Lys	Ile	Gly	Thr	Phe	Met	Ile	Pro	Gly	
			260					265					270			
Lys	Glu	Lys	Gly	Gln	Ser	Leu	Thr	Val	Gly	Ala	Gly	Asp	Leu	Ala	Trp	
		275					280					285				
Ser	Ile	Ser	Ala	Thr	Thr	Lys	His	Pro	Lys	Glu	Ala	Asn	Ala	Phe	Val	
	290					295					300					
Glu	Tyr	Met	Thr	Arg	Pro	Glu	Val	Met	Gln	Lys	Tyr	Tyr	Asp	Val	Asp	
305					310					315					320	
Gly	Ser	Pro	Thr	Ala	Ile	Glu	Gly	Val	Lys	Gln	Ala	Gly	Glu	Asp	Ser	
				325					330					335		
Pro	Leu	Ala	Gly	Met	Thr	Glu	Tyr	Ala	Phe	Thr	Asp	Arg	His	Leu	Val	
			340					345					350			

09765272 1012201



Trp Leu Gln Gln Tyr Trp Thr Ser Glu Ala Asp Phe His Thr Leu Thr  
 355 360 365

Met Asn Tyr Val Leu Thr Gly Asp Lys Gln Gly Met Val Asn Asp Leu  
 370 375 380

Asn Ala Phe Phe Asn Pro Met Lys Ala Asp Val Asp  
 385 390 395

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TGGGAAAAAT TCTAGCGAAA CTAGTGGAGA TAATTGGTCA AAGTACCAGT CTAACAAGTC	60
TATTACTATT GGATTGATA GTACTTTTGT TCCAATGGGA TTTGCTCAGA AAGATGGTTC	120
TTATGCAGGA TTTGATATTG ATTTAGCTAC AGCTGTTTTT GAAAAATACG GAATCACGGT	180
AAATTGGCAA CCGATTGATT GGGATTTGAA AGAAGCTGAA TTGACAAAAG GAACGATTGA	240
TCTGATTG AATGGCTATT CCGCTACAGA CGAACGCCGT GAAAAGGTGG CTTTCAGTAA	300
CTCATATATG AAGAATGAGC AGGTATTGGT TACGAAGAAA TCATCTGGTA TCACGACTGC	360
AAAGGATATG ACTGGAAAGA CATTAGGAGC TCAAGCTGGT TCATCTGGTT ATGCGGACTT	420
TGAAGCAAAT CCAGAAATTT TGAAGAATAT TGTCGCTAAT AAGGAAGCGA ATCAATACCA	480
AACCTTTAAT GAAGCCTTGA TTGATTTGAA AAACGATCGA ATTGATGGTC TATTGATTGA	540
CCGTGTCTAT GCAAACCTATT ATTTAGAAGC AGAAGGTGTT TTAAACGATT ATAATGTCTT	600
TACAGTTGGA CTAGAAACAG AAGCTTTTGC GGTGAGGCC CGTAAGGAAG ATACAAACTT	660
GGTTAAGAAG ATAAATGAAG CTTTTTCTAG TCTTTACAAG GACGGCAAGT TCCAAGAAAT	720
CAGCCAAAAA TGGTTTGGAG AAGATGTAGC AACCAAAGAA GTAAAAGAAG GACAG	775

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Lys Asn Ser Ser Glu Thr Ser Gly Asp Asn Trp Ser Lys Tyr Gln	
1 5 10 15	
Ser Asn Lys Ser Ile Thr Ile Gly Phe Asp Ser Thr Phe Val Pro Met	

09765272.012201

09765272.012201

131

20                      25                      30

Gly Phe Ala Gln Lys Asp Gly Ser Tyr Ala Gly Phe Asp Ile Asp Leu  
           35-                      40                      45-

Ala Thr Ala Val Phe Glu Lys Tyr Gly Ile Thr Val Asn Trp Gln Pro  
           50                      55                      60

Ile Asp Trp Asp Leu Lys Glu Ala Glu Leu Thr Lys Gly Thr Ile Asp  
           65                      70                      75                      80

Leu Ile Trp Asn Gly Tyr Ser Ala Thr Asp Glu Arg Arg Glu Lys Val  
                           85                      90                      95

Ala Phe Ser Asn Ser Tyr Met Lys Asn Glu Gln Val Leu Val Thr Lys  
                           100                      105                      110

Lys Ser Ser Gly Ile Thr Thr Ala Lys Asp Met Thr Gly Lys Thr Leu  
                           115                      120                      125

Gly Ala Gln Ala Gly Ser Ser Gly Tyr Ala Asp Phe Glu Ala Asn Pro  
           130                      135                      140

Glu Ile Leu Lys Asn Ile Val Ala Asn Lys Glu Ala Asn Gln Tyr Gln  
           145                      150                      155                      160

Thr Phe Asn Glu Ala Leu Ile Asp Leu Lys Asn Asp Arg Ile Asp Gly  
                           165                      170                      175

Leu Leu Ile Asp Arg Val Tyr Ala Asn Tyr Tyr Leu Glu Ala Glu Gly  
                           180                      185                      190

Val Leu Asn Asp Tyr Asn Val Phe Thr Val Gly Leu Glu Thr Glu Ala  
                           195                      200                      205

Phe Ala Val Gly Ala Arg Lys Glu Asp Thr Asn Leu Val Lys Lys Ile  
           210                      215                      220

Asn Glu Ala Phe Ser Ser Leu Tyr Lys Asp Gly Lys Phe Gln Glu Ile  
           225                      230                      235                      240

Ser Gln Lys Trp Phe Gly Glu Asp Val Ala Thr Lys Glu Val Lys Glu  
                           245                      250                      255

Gly Gln

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGCTAGCGGA AAAAAAGATA CAACTTCTGG TCAAAACTA AAAGTTGTTG CTACAAACTC 60

AATCATCGCT GATATTACTA AAAATATTGC TGGTGACAAA ATTGACCTTC ATAGTATCGT 120

TCCGATTGGG CAAGACCCAC ACGAATACGA ACCACTTCCT GAAGACGTTA AGAAAACTTC 180  
 TGAGGCTAAT TTGATTTTCT ATAACGGTAT CAACCTTGAA ACAGGTGGCA ATGCTTGGTT 240  
 TACAAAATTG GTAGAAAATG CCAAGAAAAC TGAAAACAAA GACTACTTCG CAGTCAGCGA 300  
 CGGCGTTGAT GTTATCTACC TTGAAGGTCA AAATGAAAAA GGAAAAGAAG ACCCACACGC 360  
 TTGGCTTAAC CTTGAAAACG GTATTATTTT TGCTAAAAAT ATCGCCAAAC AATTGAGCGC 420  
 CAAAGACCCT AACAAATAAG AATTCTATGA AAAAAATCTC AAAGAATATA CTGATAAGTT 480  
 AGACAAACTT GATAAAGAAA GTAAGGATAA ATTTAATAAG ATCCCTGCTG AAAAGAAACT 540  
 CATTGTAACC AGCGAAGGAG CATTCAAATA CTTCTCTAAA GCCTATGGTG TCCCAAGTGC 600  
 TTACATCTGG GAAATCAATA CTGAAGAAGA AGGAATCCTT GAACAAATCA AGACCTTGGT 660  
 TGAAAACTT CGCCAAACAA AAGTTCCATC ACTCTTTGTA GAATCAAGTG TGGATGACCG 720  
 TCCAATGAAA ACTGTTTCTC AAGACACAAA CATCCCAATC TACGCTCAA TCTTTACTGA 780  
 CTCTATCGCA GAACAAGGTA AAGAAGGCGA CAGCTACTAC AGCATGATGA AATACAACCT 840  
 TGACAAGATT GCTGAAGGAT TGGCAAAA 868

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Ser Gly Lys Lys Asp Thr Thr Ser Gly Gln Lys Leu Lys Val Val  
 1 5 10 15  
 Ala Thr Asn Ser Ile Ile Ala Asp Ile Thr Lys Asn Ile Ala Gly Asp  
 20 25 30  
 Lys Ile Asp Leu His Ser Ile Val Pro Ile Gly Gln Asp Pro His Glu  
 35 40 45  
 Tyr Glu Pro Leu Pro Glu Asp Val Lys Lys Thr Ser Glu Ala Asn Leu  
 50 55 60  
 Ile Phe Tyr Asn Gly Ile Asn Leu Glu Thr Gly Gly Asn Ala Trp Phe  
 65 70 75 80  
 Thr Lys Leu Val Glu Asn Ala Lys Lys Thr Glu Asn Lys Asp Tyr Phe  
 85 90 95  
 Ala Val Ser Asp Gly Val Asp Val Ile Tyr Leu Glu Gly Gln Asn Glu  
 100 105 110  
 Lys Gly Lys Glu Asp Pro His Ala Trp Leu Asn Leu Glu Asn Gly Ile  
 115 120 125

09765272 012201

Ile Phe Ala Lys Asn Ile Ala Lys Gln Leu Ser Ala Lys Asp Pro Asn  
 130 135 140  
 Asn Lys Glu Phe Tyr Glu Lys Asn Leu Lys Glu Tyr Thr Asp Lys Leu  
 145 150 155 160  
 Asp Lys Leu Asp Lys Glu Ser Lys Asp Lys Phe Asn Lys Ile Pro Ala  
 165 170 175  
 Glu Lys Lys Leu Ile Val Thr Ser Glu Gly Ala Phe Lys Tyr Phe Ser  
 180 185 190  
 Lys Ala Tyr Gly Val Pro Ser Ala Tyr Ile Trp Glu Ile Asn Thr Glu  
 195 200 205  
 Glu Glu Gly Thr Pro Glu Gln Ile Lys Thr Leu Val Glu Lys Leu Arg  
 210 215 220  
 Gln Thr Lys Val Pro Ser Leu Phe Val Glu Ser Ser Val Asp Asp Arg  
 225 230 235 240  
 Pro Met Lys Thr Val Ser Gln Asp Thr Asn Ile Pro Ile Tyr Ala Gln  
 245 250 255  
 Ile Phe Thr Asp Ser Ile Ala Glu Gln Gly Lys Glu Gly Asp Ser Tyr  
 260 265 270  
 Tyr Ser Met Met Lys Tyr Asn Leu Asp Lys Ile Ala Glu Gly Leu Ala  
 275 280 285

Lys

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1546 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGGCTCAAAA AATACAGCTT CAAGTCCAGA TTATAAGTTG GAAGGTGTAA CATTCCCGCT	60
TCAAGAAAAG AAAACATTGA AGTTTATGAC AGCCAGTTCA CCGTTATCTC CTAAAGACCC	120
AAATGAAAAG TTAATTTTGC AACGTTTGGA GAAGGAAACT GCGGTTTCATA TTGACTGGAC	180
CAACTACCAA TCCGACTTTG CAGAAAAACG TAACTTGGAT ATTTCTAGTG GTGATTTACC	240
AGATGCTATC CACAACGACG GAGCTTCAGA TGTGGACTTG ATGAACTGGG CTAAAAAAGG	300
TGTTATTATT CCAAGTTGAAG ATTTGATTGA TAAATACATG CCAAATCTTA AGAAAATTTT	360
GGATGAGAAA CCAGAGTACA AGGCCTTGAT GACAGCACCT GATGGGCACA TTTACTCATT	420
TCCATGGATT GAAGAGCTTG GAGATGGTAA AGAGTCTATT CACAGTGTC ACGATATGGC	480
TTGGATTAAC AAAGATTGGC TTAAGAAACT TGGTCTTGAA ATGCCAAAAA CTA CTGATGA	540

09765272.012201

```

TTTGATTAAA GTCCTAGAAG CTTTCAAAAA CGGGGATCCA AATGGAAATG GAGAGGCTGA      600
TGAAATTCCA TTTTCATTTA TTAGTGGTAA CGGAAACGAA GATTTTAAAT TCCTATTTGC      660
TGCATTTGGT ATAGGGGATA ACGATGATCA TTTAGTAGTA GGAAATGATG GCAAAGTTGA      720
CTTCACAGCA GATAACGATA ACTATAAAGA AGGTGTCAAA TTTATCCGTC AATTGCAAGA      780
AAAAGGCCTG ATTGATAAAG AAGCTTTTCGA ACATGATTGG AATAGTTACA TTGCTAAAGG      840
TCATGATCAG AAATTTGGTG TTTACTTTAC ATGGGATAAG AATAATGTTA CTGGAAGTAA      900
CGAAAGTTAT GATGTTTTAC CAGTACTTGC TGGACCAAGT GGTCAAAAAC ACGTAGCTCG      960
TACAAACGGT ATGGGATTTG CACGTGACAA GATGGTTATT ACCAGTGTA AAAAAACCT     1020
AGAATTGACA GCTAAATGGA TTGATGCACA ATACGCTCCA CTCCAATCTG TGCAAAATAA     1080
CTGGGGAAC TACGGAGATG ACAAACAACA AAACATCTTT GAATTGGATC AAGCGTCAAA     1140
TAGTCTAAAA CACTTACCAC TAAACGGAAC TGCACCAGCA GAACTTCGTC AAAAGACTGA     1200
AGTAGGAGGA CCACTAGCTA TCCTAGATTC ATACTATGGT AAAGTAACAA CCATGCCTGA     1260
TGATGCCAAA TGGCGTTTGG ATCTTATCAA AGAATATTAT GTTCCTTACA TGAGCAATGT     1320
CAATAACTAT CCAAGAGTCT TTATGACACA GGAAGATTTG GACAAGATTG CCCATATCGA     1380
AGCAGATATG AATGACTATA TCTACCGTAA ACGTGCTGAA TGGATTGTAA ATGGCAATAT     1440
TGATACTGAG TGGGATGATT ACAAGAAAGA ACTTGAAAAA TACGGACTTT CTGATTACCT     1500
CGCTATTAAA CAAAATACT ACGACCAATA CCAAGCAAAC AAAAAC                      1546

```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Gly Ser Lys Asn Thr Ala Ser Ser Pro Asp Tyr Lys Leu Glu Gly Val
1           5           10           15
Thr Phe Pro Leu Gln Glu Lys Lys Thr Leu Lys Phe Met Thr Ala Ser
20           25           30
Ser Pro Leu Ser Pro Lys Asp Pro Asn Glu Lys Leu Ile Leu Gln Arg
35           40           45
Leu Glu Lys Glu Thr Gly Val His Ile Asp Trp Thr Asn Tyr Gln Ser
50           55           60
Asp Phe Ala Glu Lys Arg Asn Leu Asp Ile Ser Ser Gly Asp Leu Pro
65           70           75           80
Asp Ala Ile His Asn Asp Gly Ala Ser Asp Val Asp Leu Met Asn Trp

```

09765272.012201

135

85

90

95

Ala	Lys	Lys	Gly	Val	Ile	Ile	Pro	Val	Glu	Asp	Leu	Ile	Asp	Lys	Tyr		
			100					105					110				
Met	Pro	Asn	Leu	Lys	Lys	Ile	Leu	Asp	Glu	Lys	Pro	Glu	Tyr	Lys	Ala		
		115					120					125					
Leu	Met	Thr	Ala	Pro	Asp	Gly	His	Ile	Tyr	Ser	Phe	Pro	Trp	Ile	Glu		
	130					135					140						
Glu	Leu	Gly	Asp	Gly	Lys	Glu	Ser	Ile	His	Ser	Val	Asn	Asp	Met	Ala		
145					150					155					160		
Trp	Ile	Asn	Lys	Asp	Trp	Leu	Lys	Lys	Leu	Gly	Leu	Glu	Met	Pro	Lys		
			165						170					175			
Thr	Thr	Asp	Asp	Leu	Ile	Lys	Val	Leu	Glu	Ala	Phe	Lys	Asn	Gly	Asp		
		180						185					190				
Pro	Asn	Gly	Asn	Gly	Glu	Ala	Asp	Glu	Ile	Pro	Phe	Ser	Phe	Ile	Ser		
		195					200					205					
Gly	Asn	Gly	Asn	Glu	Asp	Phe	Lys	Phe	Leu	Phe	Ala	Ala	Phe	Gly	Ile		
	210					215					220						
Gly	Asp	Asn	Asp	Asp	His	Leu	Val	Val	Gly	Asn	Asp	Gly	Lys	Val	Asp		
225					230					235					240		
Phe	Thr	Ala	Asp	Asn	Asp	Asn	Tyr	Lys	Glu	Gly	Val	Lys	Phe	Ile	Arg		
			245						250					255			
Gln	Leu	Gln	Glu	Lys	Gly	Leu	Ile	Asp	Lys	Glu	Ala	Phe	Glu	His	Asp		
			260					265					270				
Trp	Asn	Ser	Tyr	Ile	Ala	Lys	Gly	His	Asp	Gln	Lys	Phe	Gly	Val	Tyr		
		275					280					285					
Phe	Thr	Trp	Asp	Lys	Asn	Asn	Val	Thr	Gly	Ser	Asn	Glu	Ser	Tyr	Asp		
	290					295					300						
Val	Leu	Pro	Val	Leu	Ala	Gly	Pro	Ser	Gly	Gln	Lys	His	Val	Ala	Arg		
305					310					315					320		
Thr	Asn	Gly	Met	Gly	Phe	Ala	Arg	Asp	Lys	Met	Val	Ile	Thr	Ser	Val		
			325						330					335			
Asn	Lys	Asn	Leu	Glu	Leu	Thr	Ala	Lys	Trp	Ile	Asp	Ala	Gln	Tyr	Ala		
			340					345					350				
Pro	Leu	Gln	Ser	Val	Gln	Asn	Asn	Trp	Gly	Thr	Tyr	Gly	Asp	Asp	Lys		
		355					360					365					
Gln	Gln	Asn	Ile	Phe	Glu	Leu	Asp	Gln	Ala	Ser	Asn	Ser	Leu	Lys	His		
	370					375					380						
Leu	Pro	Leu	Asn	Gly	Thr	Ala	Pro	Ala	Glu	Leu	Arg	Gln	Lys	Thr	Glu		
385					390					395					400		
Val	Gly	Gly	Pro	Leu	Ala	Ile	Leu	Asp	Ser	Tyr	Tyr	Gly	Lys	Val	Thr		
			405						410					415			
Thr	Met	Pro	Asp	Asp	Ala	Lys	Trp	Arg	Leu	Asp	Leu	Ile	Lys	Glu	Tyr		

09765272.012204

136

420

425

430

Tyr Val Pro Tyr Met Ser Asn Val Asn Asn Tyr Pro Arg Val Phe Met  
435 440 445

Thr Gln Glu Asp Leu Asp Lys Ile Ala His Ile Glu Ala Asp Met Asn  
450 455 460

Asp Tyr Ile Tyr Arg Lys Arg Ala Glu Trp Ile Val Asn Gly Asn Ile  
465 470 475 480

Asp Thr Glu Trp Asp Asp Tyr Lys Lys Glu Leu Glu Lys Tyr Gly Leu  
485 490 495

Ser Asp Tyr Leu Ala Ile Lys Gln Lys Tyr Tyr Asp Gln Tyr Gln Ala  
500 505 510

Asn Lys Asn  
515

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TAGTACAAAC TCAAGCACTA GTCAGACAGA GACCAGTAGC TCTGCTCCAA CAGAGGTAAC	60
CATTAAAAGT TCACTGGACG AGGTCAAACCT TTCCAAAGTT CCTGAAAAGA TTGTGACCTT	120
TGACCTCGGC GCTGCGGATA CTATTCGCGC TTTAGGATTT GAAAAAATA TCGTCGGAAT	180
GCCTACAAAA ACTGTTCCGA CTTATCTAAA AGACCTAGTG GGAAGTGTCA AAAATGTTGG	240
TTCTATGAAA GAACCTGATT TAGAAGCTAT CGCCGCCCTT GAGCCTGATT TGATTATCGC	300
TTCGCCACGT ACACAAAAAT TCGTAGACAA ATTCAAAGAA ATCGCCCCAA CCGTTCTCTT	360
CCAAGCAAGC AAGGACGACT ACTGGACTTC TACCAAGGCT AATATCGAAT CCTTAGCAAG	420
TGCCTTCGGC GAAACTGGTA CACAGAAAGC CAAGGAAGAA TTGACCAAGC TAGACAAGAG	480
CATCCAAGAA GTCGCTACTA AAAATGAAAG CTCTGACAAA AAAGCCCTTG CGATCCTCCT	540
TAATGAAGGA AAAATGGCAG CCTTTGGTGC CAAATCTCGT TTCTCTTTCT TGTACCAAAC	600
CTTGAAATTC AAACCAACTG ATACAAAATT TGAAGACTCA CGCCACGGAC AAGAAGTCAG	660
CTTTGAAAGT GTCAAAGAAA TCAACCCTGA CATCCTCTTT GTCATCAACC GTACCCTTGC	720
CATCGGTGGG GACAACTCTA GCAACGACGG TGTCCTAGAA AATGCCCTTA TCGCTGAAAC	780
ACCTGCTGCT AAAAATGGTA AGATTATCCA ACTAACACCA GACCTCTGGT ATCTAAGCGG	840
AGGCGGACTT GAATCAACAA AACTCATGAT TGAAGACATA CAAAAGCTT TGAAA	895

(2) INFORMATION FOR SEQ ID NO: 24:

00765272.012201

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser	Thr	Asn	Ser	Ser	Thr	Ser	Gln	Thr	Glu	Thr	Ser	Ser	Ser	Ala	Pro	1	5	10	15
Thr	Glu	Val	Thr	Ile	Lys	Ser	Ser	Leu	Asp	Glu	Val	Lys	Leu	Ser	Lys	20	25	30	
Val	Pro	Glu	Lys	Ile	Val	Thr	Phe	Asp	Leu	Gly	Ala	Ala	Asp	Thr	Ile	35	40	45	
Arg	Ala	Leu	Gly	Phe	Glu	Lys	Asn	Ile	Val	Gly	Met	Pro	Thr	Lys	Thr	50	55	60	
Val	Pro	Thr	Tyr	Leu	Lys	Asp	Leu	Val	Gly	Thr	Val	Lys	Asn	Val	Gly	65	70	75	80
Ser	Met	Lys	Glu	Pro	Asp	Leu	Glu	Ala	Ile	Ala	Ala	Leu	Glu	Pro	Asp	85	90	95	
Leu	Ile	Ile	Ala	Ser	Pro	Arg	Thr	Gln	Lys	Phe	Val	Asp	Lys	Phe	Lys	100	105	110	
Glu	Ile	Ala	Pro	Thr	Val	Leu	Phe	Gln	Ala	Ser	Lys	Asp	Asp	Tyr	Trp	115	120	125	
Thr	Ser	Thr	Lys	Ala	Asn	Ile	Glu	Ser	Leu	Ala	Ser	Ala	Phe	Gly	Glu	130	135	140	
Thr	Gly	Thr	Gln	Lys	Ala	Lys	Glu	Glu	Leu	Thr	Lys	Leu	Asp	Lys	Ser	145	150	155	160
Ile	Gln	Glu	Val	Ala	Thr	Lys	Asn	Glu	Ser	Asp	Lys	Lys	Ala	Leu	165	170	175		
Ala	Ile	Leu	Leu	Asn	Glu	Gly	Lys	Met	Ala	Ala	Phe	Gly	Ala	Lys	Ser	180	185	190	
Arg	Phe	Ser	Phe	Leu	Tyr	Gln	Thr	Leu	Lys	Phe	Lys	Pro	Thr	Asp	Thr	195	200	205	
Lys	Phe	Glu	Asp	Ser	Arg	His	Gly	Gln	Glu	Val	Ser	Phe	Glu	Ser	Val	210	215	220	
Lys	Glu	Ile	Asn	Pro	Asp	Ile	Leu	Phe	Val	Ile	Asn	Arg	Thr	Leu	Ala	225	230	235	240
Ile	Gly	Gly	Asp	Asn	Ser	Ser	Asn	Asp	Gly	Val	Leu	Glu	Asn	Ala	Leu	245	250	255	
Ile	Ala	Glu	Thr	Pro	Ala	Ala	Lys	Asn	Gly	Lys	Ile	Ile	Gln	Leu	Thr	260	265	270	

09765272.012201



Pro Asp Leu Trp Tyr Leu Ser Gly Gly Gly Leu Glu Ser Thr Lys Leu  
 275 280 285

Met Ile Glu Asp Ile Gln Lys Ala Leu Lys  
 290 295

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TGGCAATTCT GCGGAAGTA AAGATGCTGC CAAATCAGGT GGTGACGGTG CAAAACAGA	60
AATCACTTGG TGGGCATTCC CAGTATTTAC CCAAGAAAAA ACTGGTGACG GTGTTGGAAC	120
TTATGAAAAA TCAATCATCG AAGCGTTTGA AAAAGCAAAC CCAGATATAA AAGTGAAATT	180
GGAAACCATC GACTTCAAGT CAGGTCCTGA AAAAATCACA ACAGCCATCG AAGCAGGAAC	240
AGCTCCAGAC GTACTCTTTG ATGCACCAGG ACGTATCATC CAATACGGTA AAAACGGTAA	300
ATTGGCTGAG TTGAATGACC TCTTCACAGA TGAATTTGTT AAAGATGTCA ACAATGAAAA	360
CATCGTACAA GCAAGTAAAG CTGGAGACAA GGCTTATATG TATCCGATTA GTTCTGCCCC	420
ATTCTACATG GCAATGAACA AGAAAATGTT AGAAGATGCT GGAGTAGCAA ACCTTGTAAG	480
AGAAGGTTGG ACAACTGATG ATTTTGAAAA AGTATTGAAA GCACTTAAAG ACAAGGGTTA	540
CACACCAGGT TCATTGTTCA GTTCTGGTCA AGGGGGAGAC CAAGGAACAC GTGCCTTTAT	600
CTCTAACCTT TATAGCGGTT CTGTAACAGA TGAAAAAGTT AGCAAATATA CAACTGATGA	660
TCCTAAATTC GTCAAAGGTC TTGAAAAAGC AACTAGCTGG ATTAAAGACA ATTTGATCAA	720
TAATGGTTCA CAATTTGACG GTGGGGCAGA TATCCAAAAC TTTGCCAACG GTCAAACATC	780
TTACACAATC CTTTGGGCAC CAGCTCAAAA TGGTATCCAA GCTAAACTTT TAGAAGCAAG	840
TAAGGTAGAA GTGGTAGAAG TACCATTCCC ATCAGACGAA GGTAAGCCAG CTCTTGAGTA	900
CCTTGTAAC GGGTTTGCAG TATTCAACAA TAAAGACGAC AAGAAAGTCG CTGCATCTAA	960
GAAATTCATC CAGTTTATCG CAGATGACAA GGAGTGGGGA CCTAAAGACG TAGTTCGTAC	1020
AGGTGCTTTC CCAGTCCGTA CTTCAATTTGG AAAACTTTAT GAAGACAAAC GCATGGAAAC	1080
AATCAGCGGC TGGACTCAAT ACTACTCACC ATACTACAAC ACTATTGATG GATTGCTGA	1140
AATGAGAACA CTTTGGTTCC CAATGTTGCA ATCTGTATCA AATGGTGACG AAAAACCAGC	1200
AGATGCTTTG AAAGCCTTCA CTGAAAAAGC GAACGAAACA ATCAAAAAAG CTATGAAACA	1260
A	1261

(2) INFORMATION FOR SEQ ID NO: 26:

09765272.012201

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly	Asn	Ser	Gly	Gly	Ser	Lys	Asp	Ala	Ala	Lys	Ser	Gly	Gly	Asp	Gly				
1				5					10					15					
Ala	Lys	Thr	Glu	Ile	Thr	Trp	Trp	Ala	Phe	Pro	Val	Phe	Thr	Gln	Glu				
			20					25					30						
Lys	Thr	Gly	Asp	Gly	Val	Gly	Thr	Tyr	Glu	Lys	Ser	Ile	Ile	Glu	Ala				
		35					40					45							
Phe	Glu	Lys	Ala	Asn	Pro	Asp	Ile	Lys	Val	Lys	Leu	Glu	Thr	Ile	Asp				
	50					55					60								
Phe	Lys	Ser	Gly	Pro	Glu	Lys	Ile	Thr	Thr	Ala	Ile	Glu	Ala	Gly	Thr				
65					70					75					80				
Ala	Pro	Asp	Val	Leu	Phe	Asp	Ala	Pro	Gly	Arg	Ile	Ile	Gln	Tyr	Gly				
			85						90					95					
Lys	Asn	Gly	Lys	Leu	Ala	Glu	Leu	Asn	Asp	Leu	Phe	Thr	Asp	Glu	Phe				
			100					105					110						
Val	Lys	Asp	Val	Asn	Asn	Glu	Asn	Ile	Val	Gln	Ala	Ser	Lys	Ala	Gly				
		115				120						125							
Asp	Lys	Ala	Tyr	Met	Tyr	Pro	Ile	Ser	Ser	Ala	Pro	Phe	Tyr	Met	Ala				
	130					135					140								
Met	Asn	Lys	Lys	Met	Leu	Glu	Asp	Ala	Gly	Val	Ala	Asn	Leu	Val	Lys				
145					150					155					160				
Glu	Gly	Trp	Thr	Thr	Asp	Asp	Phe	Glu	Lys	Val	Leu	Lys	Ala	Leu	Lys				
			165						170					175					
Asp	Lys	Gly	Tyr	Thr	Pro	Gly	Ser	Leu	Phe	Ser	Ser	Gly	Gln	Gly	Gly				
		180						185					190						
Asp	Gln	Gly	Thr	Arg	Ala	Phe	Ile	Ser	Asn	Leu	Tyr	Ser	Gly	Ser	Val				
		195					200					205							
Thr	Asp	Glu	Lys	Val	Ser	Lys	Tyr	Thr	Thr	Asp	Asp	Pro	Lys	Phe	Val				
	210					215					220								
Lys	Gly	Leu	Glu	Lys	Ala	Thr	Ser	Trp	Ile	Lys	Asp	Asn	Leu	Ile	Asn				
225					230					235				240					
Asn	Gly	Ser	Gln	Phe	Asp	Gly	Gly	Ala	Asp	Ile	Gln	Asn	Phe	Ala	Asn				
			245					250					255						
Gly	Gln	Thr	Ser	Tyr	Thr	Ile	Leu	Trp	Ala	Pro	Ala	Gln	Asn	Gly	Ile				
		260						265					270						

09765272.012201

Gln Ala Lys Leu Leu Glu Ala Ser Lys Val Glu Val Val Glu Val Pro  
275 280 285

Phe Pro Ser Asp Glu Gly Lys Pro Ala Leu Glu Tyr Leu Val Asn Gly  
290 295 300

Phe Ala Val Phe Asn Asn Lys Asp Asp Lys Lys Val Ala Ala Ser Lys  
305 310 315 320

Lys Phe Ile Gln Phe Ile Ala Asp Asp Lys Glu Trp Gly Pro Lys Asp  
325 330 335

Val Val Arg Thr Gly Ala Phe Pro Val Arg Thr Ser Phe Gly Lys Leu  
340 345 350

Tyr Glu Asp Lys Arg Met Glu Thr Ile Ser Gly Trp Thr Gln Tyr Tyr  
355 360 365

Ser Pro Tyr Tyr Asn Thr Ile Asp Gly Phe Ala Glu Met Arg Thr Leu  
370 375 380

Trp Phe Pro Met Leu Gln Ser Val Ser Asn Gly Asp Glu Lys Pro Ala  
385 390 395 400

Asp Ala Leu Lys Ala Phe Thr Glu Lys Ala Asn Glu Thr Ile Lys Lys  
405 410 415

Ala Met Lys Gln  
420

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TTCACAAGAA AAAACAAAA ATGAAGATGG AGAACTAAG ACAGAACAGA CAGCCAAAGC	60
TGATGGAACA GTCGGTAGTA AGTCTCAAGG AGCTGCCCAG AAGAAAGCAG AAGTGGTCAA	120
TAAAGGTGAT TACTACAGCA TTCAAGGGAA ATACGATGAA ATCATCGTAG CCAACAAACA	180
CTATCCATTG TCTAAAGACT ATAATCCAGG GGAAAATCCA ACAGCCAAGG CAGAGTTGGT	240
CAAATCATC AAAGCGATGC AAGAGGCAGG TTTCCCTATT AGTGATCATT ACAGTGGTTT	300
TAGAAGTTAT GAAACTCAGA CCAAGCTCTA TCAAGATTAT GTCAACCAAG ATGGAAAGGC	360
AGCAGCTGAC CGTTACTCTG CCCGTCCTGG CTATAGCGAA CACCAGACAG GCTTGGCCTT	420
TGATGTGATT GGGACTGATG GTGATTTGGT GACAGAAGAA AAAGCAGCCC AATGGCTCTT	480
GGATCATGCA GCTGATTATG GCTTTGTTGT CCGTTATCTC AAAGGCAAGG AAAAGGAAAC	540
AGGCTATATG GCTGAAGAAT GGCACCTGCG TTATGTAGGA AAAGAAGCTA AAGAAATTGC	600
TGCAAGTGGT CTCAGTTTGG AAGAATACTA TGGCTTTGAA GGCGGAGACT ACGTCGAT	658

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Ser Gln Glu Lys Thr Lys Asn Glu Asp Gly Glu Thr Lys Thr Glu Gln
1      5      10      15
Thr Ala Lys Ala Asp Gly Thr Val Gly Ser Lys Ser Gln Gly Ala Ala
20      25      30
Gln Lys Lys Ala Glu Val Val Asn Lys Gly Asp Tyr Tyr Ser Ile Gln
35      40      45
Gly Lys Tyr Asp Glu Ile Ile Val Ala Asn Lys His Tyr Pro Leu Ser
50      55      60
Lys Asp Tyr Asn Pro Gly Glu Asn Pro Thr Ala Lys Ala Glu Leu Val
65      70      75      80
Lys Leu Ile Lys Ala Met Gln Glu Ala Gly Phe Pro Ile Ser Asp His
85      90      95
Tyr Ser Gly Phe Arg Ser Tyr Glu Thr Gln Thr Lys Leu Tyr Gln Asp
100     105     110
Tyr Val Asn Gln Asp Gly Lys Ala Ala Asp Arg Tyr Ser Ala Arg
115     120     125
Pro Gly Tyr Ser Glu His Gln Thr Gly Leu Ala Phe Asp Val Ile Gly
130     135     140
Thr Asp Gly Asp Leu Val Thr Glu Glu Lys Ala Ala Gln Trp Leu Leu
145     150     155     160
Asp His Ala Ala Asp Tyr Gly Phe Val Val Arg Tyr Leu Lys Gly Lys
165     170     175
Glu Lys Glu Thr Gly Tyr Met Ala Glu Glu Trp His Leu Arg Tyr Val
180     185     190
Gly Lys Glu Ala Lys Glu Ile Ala Ala Ser Gly Leu Ser Leu Glu Glu
195     200     205
Tyr Tyr Gly Phe Glu Gly Gly Asp Tyr Val Asp
210     215

```

## (2) INFORMATION FOR SEQ ID NO: 29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

09765272-012201

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GAAAGGTCTG TGGTCAAATA ATCTTACCTG CGGTTATGAT GAAAAAATAA TCTTGAAAA 60  
TATAAATATA AAAATACCTG AAGAAAAAAT ATCAGTTATT ATTGGGTCAA ATGGTTGTGG 120  
GAAATCAACA CTCATTAAAA CCTTGTCTCG ACTTATAAAG CCATTAGAGG GAGAAGTATT 180  
GCTTGATAAT AAATCAATTA ATTCTTATAA AGAAAAAGAT TTAGCAAAAC ACATAGCTAT 240  
ATTACCTCAA TCTCCAATAA TCCCTGAATC AATAACAGTA GCTGATCTTG TAAGCCGTGG 300  
TCGTTTCCCC TACAGAAAGC CTTTAAAGAG TCTTGAAAA GATGACCTTG AAATAATAAA 360  
CAGATCAATG GTTAAGGCCA ATGTTGAAGA TCTAGCAAAT AACCTAGTTG AAGAACTTTC 420  
TGGGGGTCAA AGGCAAAGAG TATGGATAGC TCTAGCCCTA GCCCAAGATA CAAGTATCCT 480  
ACTTTTAGAT GAGCCAACTA CTTACTTGGA TATCTCATAT CAAATAGAAC TATTAGACCT 540  
CTTGACTGAT CTAAACCAA AATATAAGAC AACCATTGTC ATGATTTTGC ACGATATAAA 600  
TCTAACAGCA AGATACGCTG ATTACCTATT TGCAATTAAA GAAGGTAAAC TTGTTGCAGA 660  
GGGAAAGCCT GAAGATATAC TAAATGATAA ACTAGTTAAA GATATCTTTA ATCTTGAAGC 720  
AAAAATTATA CGTGACCCTA TTTCCAATTC GCCTCTAATG ATTCCTATTG GCAAGCACCA 780  
TGTTAACCTCT 790

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Gly Leu Trp Ser Asn Asn Leu Thr Cys Gly Tyr Asp Glu Lys Ile  
1 5 10 15  
Ile Leu Glu Asn Ile Asn Ile Lys Ile Pro Glu Glu Lys Ile Ser Val  
20 25 30  
Ile Ile Gly Ser Asn Gly Cys Gly Lys Ser Thr Leu Ile Lys Thr Leu  
35 40 45  
Ser Arg Leu Ile Lys Pro Leu Glu Gly Glu Val Leu Leu Asp Asn Lys  
50 55 60  
Ser Ile Asn Ser Tyr Lys Glu Lys Asp Leu Ala Lys His Ile Ala Ile  
65 70 75 80  
Leu Pro Gln Ser Pro Ile Ile Pro Glu Ser Ile Thr Val Ala Asp Leu  
85 90 95

09765272-012201

Val Ser Arg Gly Arg Phe Pro Tyr Arg Lys Pro Phe Lys Ser Leu Gly  
100 105 110

Lys Asp Asp Leu Glu Ile Ile Asn Arg Ser Met Val Lys Ala Asn Val  
115 120 125

Glu Asp Leu Ala Asn Asn Leu Val Glu Glu Leu Ser Gly Gly Gln Arg  
130 135 140

Gln Arg Val Trp Ile Ala Leu Ala Leu Ala Gln Asp Thr Ser Ile Leu  
145 150 155 160

Leu Leu Asp Glu Pro Thr Thr Tyr Leu Asp Ile Ser Tyr Gln Ile Glu  
165 170 175

Leu Leu Asp Leu Leu Thr Asp Leu Asn Gln Lys Tyr Lys Thr Thr Ile  
180 185 190

Cys Met Ile Leu His Asp Ile Asn Leu Thr Ala Arg Tyr Ala Asp Tyr  
195 200 205

Leu Phe Ala Ile Lys Glu Gly Lys Leu Val Ala Glu Gly Lys Pro Glu  
210 215 220

Asp Ile Leu Asn Asp Lys Leu Val Lys Asp Ile Phe Asn Leu Glu Ala  
225 230 235 240

Lys Ile Ile Arg Asp Pro Ile Ser Asn Ser Pro Leu Met Ile Pro Ile  
245 250 255

Gly Lys His His Val Ser  
260

## (2) INFORMATION FOR SEQ ID NO: 31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAACTCAGAA AAGAAAGCAG ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG	60
CGGTTCTGAA GAAAAACGTT GGGACAAAAT CCAAGAATTG GTTAAAAAAG ACGGAATTAC	120
CTTGGAATTT ACAGAGTTCA CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA	180
AGTAGATTTG AACGCTTTCC AACACTATAA CTTCTTGAAC AACTGGAACA AAGAAAACGG	240
AAAAGACCTT GTAGCGATTG CAGATACTTA CATCTCTCCA ATCCGCCTTT ACTCAGGTTT	300
GAATGGAAGT GCCAACAAGT AACTAAAGT AGAAGACATC CCAGCAAACG GAGAAATCGC	360
TGTACCGAAT GACGCTACAA ACGAAAGCCG TGCCTTTTAT TTGCTTCAAT CAGCTGGCTT	420
GATTAAATTG GATGTTTCTG GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC	480
AAAGAACTTG AAAATCACTG AATTGGACGC TAGCCAAACA GTCGTTTCAT TGTCATCAGT	540

TGACGCTGCC GTTGTAACA ATACCTTCGT TACAGAAGCA AAATTGGACT ACAAGAAATC 600  
 ACTTTTCAAA GAACAAGCTG ATGAAACTC AAAACAATGG TACAACATCA TTGTTGCAAA 660  
 AAAAGATTGG GAAACATCAC CTAAGGCTGA TGCTATCAAG AAAGTAATCG CAGCTTACCA 720  
 CACAGATGAC GTGAAAAAAG TTATCGAAGA ATCATCAGAT GGT'TTGGATC AACCAGTTTG 780  
 G 781

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn	Ser	Glu	Lys	Lys	Ala	Asp	Asn	Ala	Thr	Thr	Ile	Lys	Ile	Ala	Thr	1	5	10	15
Val	Asn	Arg	Ser	Gly	Ser	Glu	Glu	Lys	Arg	Trp	Asp	Lys	Ile	Gln	Glu	20	25	30	
Leu	Val	Lys	Lys	Asp	Gly	Ile	Thr	Leu	Glu	Phe	Thr	Glu	Phe	Thr	Asp	35	40	45	
Tyr	Ser	Gln	Pro	Asn	Lys	Ala	Thr	Ala	Asp	Gly	Glu	Val	Asp	Leu	Asn	50	55	60	
Ala	Phe	Gln	His	Tyr	Asn	Phe	Leu	Asn	Asn	Trp	Asn	Lys	Glu	Asn	Gly	65	70	75	80
Lys	Asp	Leu	Val	Ala	Ile	Ala	Asp	Thr	Tyr	Ile	Ser	Pro	Ile	Arg	Leu	85	90	95	
Tyr	Ser	Gly	Leu	Asn	Gly	Ser	Ala	Asn	Lys	Tyr	Thr	Lys	Val	Glu	Asp	100	105	110	
Ile	Pro	Ala	Asn	Gly	Glu	Ile	Ala	Val	Pro	Asn	Asp	Ala	Thr	Asn	Glu	115	120	125	
Ser	Arg	Ala	Leu	Tyr	Leu	Leu	Gln	Ser	Ala	Gly	Leu	Ile	Lys	Leu	Asp	130	135	140	
Val	Ser	Gly	Thr	Ala	Leu	Ala	Thr	Val	Ala	Asn	Ile	Lys	Glu	Asn	Pro	145	150	155	160
Lys	Asn	Leu	Lys	Ile	Thr	Glu	Leu	Asp	Ala	Ser	Gln	Thr	Ala	Arg	Ser	165	170	175	
Leu	Ser	Ser	Val	Asp	Ala	Ala	Val	Val	Asn	Asn	Thr	Phe	Val	Thr	Glu	180	185	190	
Ala	Lys	Leu	Asp	Tyr	Lys	Lys	Ser	Leu	Phe	Lys	Glu	Gln	Ala	Asp	Glu	195	200	205	

09765272.012201

Asn Ser Lys Gln Trp Tyr Asn Ile Ile Val Ala Lys Lys Asp Trp Glu  
 210 215 220

Thr Ser Pro Lys Ala Asp Ala Ile Lys Lys Val Ile Ala Ala Tyr His  
 225 230 235 240

Thr Asp Asp Val Lys Lys Val Ile Glu Glu Ser Ser Asp Gly Leu Asp  
 245 250 255

Gln Pro Val Trp  
 260

## (2) INFORMATION FOR SEQ ID NO: 33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TTCGAAAGGG TCAGAAGGTG CAGACCTTAT CAGCATGAAA GGGGATGTCA TTACAGAACA	60
TCAATTTTAT GAGCAAGTGA AAAGCAACCC TTCAGCCCAA CAAGTCTTGT TAAATATGAC	120
CATCCAAAAA GTTTTTGAAA AACAATATGG CTCAGAGCTT GATGATAAAG AGGTTGATGA	180
TACTATTGCC GAAGAAAAAA AACAATATGG CGAAAACTAC CAACGTGTCT TGTCACAAGC	240
AGGTATGACT CTTGAAACAC GTAAAGCTCA AATTCGTACA AGTAAATTAG TTGAGTTGGC	300
AGTTAAGAAG GTAGCAGAAG CTGAATTGAC AGATGAAGCC TATAAGAAAG CCTTTGATGA	360
GTACACTCCA GATGTAACGG CTCAAATCAT CCGTCTTAAT AATGAAGATA AGGCCAAAGA	420
AGTTCTCGAA AAAGCCAAGG CAGAAGGTGC TGATTTTGCT CAATTAGCCA AAGATAATTC	480
AACTGATGAA AAAACAAAAG AAAATGGTGG AGAAATTACC TTTGATTCTG CTTCAACAGA	540
AGTACCTGGA GCAAGTCCAA AAAAGCCGCT TTTCGCTTTT AGATGTGGGA TGGTGTCTCT	600
GGATGTGGAT TACAGCAACT GGGGCACACC AAGCCTACAG	640

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Lys Gly Ser Glu Gly Ala Asp Leu Ile Ser Met Lys Gly Asp Val	
1 5 10 15	
Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys Ser Asn Pro Ser Ala	

09765272.012201



09765272 012201

146

20	25	30
Gln Gln Val Leu Leu Asn Met Thr Ile Gln Lys Val Phe Glu Lys Gln		
35	40	45
Tyr Gly Ser Glu Leu Asp Asp Lys Glu Val Asp Asp Thr Ile Ala Glu		
50	55	60
Glu Lys Lys Gln Tyr Gly Glu Asn Tyr Gln Arg Val Leu Ser Gln Ala		
65	70	75
Gly Met Thr Leu Glu Thr Arg Lys Ala Gln Ile Arg Thr Ser Lys Leu		
85	90	95
Val Glu Leu Ala Val Lys Lys Val Ala Glu Ala Glu Leu Thr Asp Glu		
100	105	110
Ala Tyr Lys Lys Ala Phe Asp Glu Tyr Thr Pro Asp Val Thr Ala Gln		
115	120	125
Ile Ile Arg Leu Asn Asn Glu Asp Lys Ala Lys Glu Val Leu Glu Lys		
130	135	140
Ala Lys Ala Glu Gly Ala Asp Phe Ala Gln Leu Ala Lys Asp Asn Ser		
145	150	155
Thr Asp Glu Lys Thr Lys Glu Asn Gly Gly Glu Ile Thr Phe Asp Ser		
165	170	175
Ala Ser Thr Glu Val Pro Gly Ala Ser Pro Lys Lys Pro Leu Phe Ala		
180	185	190
Phe Arg Cys Gly Met Val Phe Leu Asp Val Asp Tyr Ser Asn Trp Gly		
195	200	205
Thr Pro Ser Leu Gln		
210		

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 631 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGGGATGGCA GCTTTTAAAA ATCCTAACAA TCAATACAAA GCTATTACAA TTGCTCAAAC	60
TCTAGGTGAT GATGCTTCTT CAGAGGAATT GGCTGGTAGA TATGGTTCTG CTGTTTCAGTG	120
TACAGAAGTG ACTGCCTCAA ACCTTTCAAC AGTTAAAACT AAAGCTACGG TTGTAGAAAA	180
ACCACTGAAA GATTTTtagag CGTCTACGTC TGATCAGTCT GGTTGGGTGG AATCTAATGG	240
TAAATGGTAT TTCTATGAGT CTGGTGATGT GAAGACAGGT TGGGTGAAAA CAGATGGTAA	300
ATGGTACTAT TTGAATGACT TAGGTGTCAT GCAGACTGGA TTTGTAAAAT TTTCTGGTAG	360
CTGGTATTAC TTGAGCAATT CAGGTGCTAT GTTTACAGGC TGGGGAACAG ATGGTAGCAG	420

ATGGTTCCTAC TTTGACGGCT CAGGAGCTAT GAAGACAGGC TGGTACAAGG AAAATGGCAC 480  
 TTGGTATTAC CTTGACGAAG CAGGTATCAT GAAGACAGGT TGGTTTAAAG TCGGACCACA 540  
 CTGGTACTAT GCCTACGGTT CAGGAGCTTT GGCTGTGAGC ACAACAACAC CAGATGGTTA 600  
 CCGTGTAAT GGTAATGGTG AATGGGTAAA C 631

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Met Ala Ala Phe Lys Asn Pro Asn Asn Gln Tyr Lys Ala Ile Thr  
 1 5 10 15  
 Ile Ala Gln Thr Leu Gly Asp Asp Ala Ser Ser Glu Glu Leu Ala Gly  
 20 25 30  
 Arg Tyr Gly Ser Ala Val Gln Cys Thr Glu Val Thr Ala Ser Asn Leu  
 35 40 45  
 Ser Thr Val Lys Thr Lys Ala Thr Val Val Glu Lys Pro Leu Lys Asp  
 50 55 60  
 Phe Arg Ala Ser Thr Ser Asp Gln Ser Gly Trp Val Glu Ser Asn Gly  
 65 70 75 80  
 Lys Trp Tyr Phe Tyr Glu Ser Gly Asp Val Lys Thr Gly Trp Val Lys  
 85 90 95  
 Thr Asp Gly Lys Trp Tyr Tyr Leu Asn Asp Leu Gly Val Met Gln Thr  
 100 105 110  
 Gly Phe Val Lys Phe Ser Gly Ser Trp Tyr Tyr Leu Ser Asn Ser Gly  
 115 120 125  
 Ala Met Phe Thr Gly Trp Gly Thr Asp Gly Ser Arg Trp Phe Tyr Phe  
 130 135 140  
 Asp Gly Ser Gly Ala Met Lys Thr Gly Trp Tyr Lys Glu Asn Gly Thr  
 145 150 155 160  
 Trp Tyr Tyr Leu Asp Glu Ala Gly Ile Met Lys Thr Gly Trp Phe Lys  
 165 170 175  
 Val Gly Pro His Trp Tyr Tyr Ala Tyr Gly Ser Gly Ala Leu Ala Val  
 180 185 190  
 Ser Thr Thr Thr Pro Asp Gly Tyr Arg Val Asn Gly Asn Gly Glu Trp  
 195 200 205  
 Val Asn  
 210

00765272.0122001

## (2) INFORMATION FOR SEQ ID NO: 37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

AGACGAGCAA AAAATTAAGC AAGCAGAAGC GGAAGTTGAG AGTAAACAAG CTGAGGCTAC	60
AAGGTTAAAA AAAATCAAGA CAGATCGTGA AGAAGCAGAA GAAGAAGCTA AACGAAGAGC	120
AGATGCTAAA GAGCAAGGTA AACCAAAGGG GCGGGCAAAA CGAGGAGTTC CTGGAGAGCT	180
AGCAACACCT GATAAAAAAG AAAATGATGC GAAGTCTTCA GATTCTAGCG TAGGTGAAGA	240
AACTCTTCCA AGCCCATCCC TGAAACCAGA AAAAAAGGTA GCAGAAGCTG AGAAGAAGGT	300
TGAAGAAGCT AAGAAAAAG CCGAGGATCA AAAAGAAGAA GATCGCCGTA ACTACCCAAC	360
CAATACTTAC AAAACGCTTG AACTTGAAAT TGCTGAGTCC GATGTGGAAG TTAAAAAAGC	420
GGAGCTTGAA CTAGTAAAAG AGGAAGCTAA GGAACCTCGA AACGAGGAAA AAGTTAAGCA	480
AGCAAAAGCG GAAGTTGAGA GTAAAAAAGC TGAGGCTACA AGGTTAGAAA AAATCAAGAC	540
AGATCGTAAA AAAGCAGAAG AAGAAGCTAA ACGAAAAGCA GCAGAAGAAG ATAAAGTTAA	600
AGAAAAACCA GCTGAACAAC CACAACCAGC GCCGGCTCCA AAAGCAGAAA AACCAGCTCC	660
AGCTCCAAAA CCAGAGAATC CAGCTGAACA ACCAAAAGCA GAAAAACCAG CTGATCAACA	720
AGCTGAAGAA GACTATGCTC GTAGATCAGA AGAAGAATAT AATCGCTTGA CTCAACAGCA	780
ACCGCCAAAA ACTGAAAAAC CAGCACAACC ATCTACTCCA AAAACAGGCT GGAAACAAGA	840
AAACGGTATG TGGTACTTCT ACAATACTGA TGGTTCAATG GCGACAGGAT GGCTCCAAAA	900
CAATGGCTCA TGGTACTACC TCAACAGCAA TGGCGCTATG GCGACAGGAT GGCTCCAAAA	960
CAATGGTTCA TGGTACTATC TAAACGCTAA TGGTTCAATG GCAACAGGAT GGCTCCAAAA	1020
CAATGGTTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA	1080
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTTCAATG GCGACAGGAT GGCTCCAATA	1140
CAATGGCTCA TGGTACTACC TAAACGCTAA TGGTGATATG GCGACAGGTT GGGTGAAAGA	1200
TGGAGATACC TGGTACTATC TTGAAGCATC AGGTGCTATG AAAGCAAGCC AATGGTTCAA	1260
AGTATCAGAT AAATGGTACT ATGTCAATGG CTCAGGTGCC CTTGCAGTCA ACACAACGTG	1320
AGATGGCTAT GGAGTCAATG CCAATGGTGA ATGGGTAAAC	1360

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids

09765272-012201

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Asp Glu Gln Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln
1      5      10      15
Ala Glu Ala Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala
20      25      30
Glu Glu Glu Ala Lys Arg Arg Ala Asp Ala Lys Glu Gln Gly Lys Pro
35      40      45
Lys Gly Arg Ala Lys Arg Gly Val Pro Gly Glu Leu Ala Thr Pro Asp
50      55      60
Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser Ser Val Gly Glu Glu
65      70      75      80
Thr Leu Pro Ser Pro Ser Leu Lys Pro Glu Lys Lys Val Ala Glu Ala
85      90      95
Glu Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu Asp Gln Lys Glu
100     105     110
Glu Asp Arg Arg Asn Tyr Pro Thr Asn Thr Tyr Lys Thr Leu Glu Leu
115     120     125
Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu Glu Leu
130     135     140
Val Lys Glu Glu Ala Lys Glu Pro Arg Asn Glu Glu Lys Val Lys Gln
145     150     155     160
Ala Lys Ala Glu Val Glu Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu
165     170     175
Lys Ile Lys Thr Asp Arg Lys Lys Ala Glu Glu Glu Ala Lys Arg Lys
180     185     190
Ala Ala Glu Glu Asp Lys Val Lys Glu Lys Pro Ala Glu Gln Pro Gln
195     200     205
Pro Ala Pro Ala Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro Lys Pro
210     215     220
Glu Asn Pro Ala Glu Gln Pro Lys Ala Glu Lys Pro Ala Asp Gln Gln
225     230     235     240
Ala Glu Glu Asp Tyr Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg Leu
245     250     255
Thr Gln Gln Gln Pro Pro Lys Thr Glu Lys Pro Ala Gln Pro Ser Thr
260     265     270
Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn
275     280     285

```

09765272.012201

Thr Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp  
290 295 300

Tyr Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Asn  
305 310 315 320

Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser Met Ala Thr Gly  
325 330 335

Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser  
340 345 350

Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn  
355 360 365

Ala Asn Gly Ser Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp  
370 375 380

Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Val Lys Asp  
385 390 395 400

Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser  
405 410 415

Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Ser Gly  
420 425 430

Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Gly Val Asn Ala Asn  
435 440 445

Gly Glu Trp Val Asn  
450

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGTGGTGAG GAAGAACTA AAAAGACTCA AGCAGCACAA CAGCCAAAAC AACAAACGAC	60
TGTACAACAA ATTGCTGTTG GAAAAGATGC TCCAGACTTC ACATTGCAAT CCATGGATGG	120
CAAAGAAGTT AAGTTATCTG ATTTTAAGGG TAAAAAGGTT TACTTGAAGT TTTGGGCTTC	180
ATGGTGTGGT CCATGCAAGA AAAGTATGCC AGAGTTGATG GAACTAGCGG CGAAACCAGA	240
TCGTGATTTC GAAATTCTTA CTGTCATTGC ACCAGGAATT CAAGGTGAAA AAAGTGTGTA	300
GCAATTCCCA CAATGGTTCC AGGAACAAGG ATATAAGGAT ATCCCAGTTC TTTATGATAC	360
CAAAGCAACC ACTTCCAAGC TTATCAAATT CGAAGCATTC CTACAGAATA TT	412

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Cys	Gly	Glu	Glu	Glu	Thr	Lys	Lys	Thr	Gln	Ala	Ala	Gln	Gln	Pro	Lys	
1				5					10					15		
Gln	Gln	Thr	Thr	Val	Gln	Gln	Ile	Ala	Val	Gly	Lys	Asp	Ala	Pro	Asp	
			20				25						30			
Phe	Thr	Leu	Gln	Ser	Met	Asp	Gly	Lys	Glu	Val	Lys	Leu	Ser	Asp	Phe	
		35					40					45				
Lys	Gly	Lys	Lys	Val	Tyr	Leu	Lys	Phe	Trp	Ala	Ser	Trp	Cys	Gly	Pro	
	50					55				60						
Cys	Lys	Lys	Ser	Met	Pro	Glu	Leu	Met	Glu	Leu	Ala	Ala	Lys	Pro	Asp	
65				70				75						80		
Arg	Asp	Phe	Glu	Ile	Leu	Thr	Val	Ile	Ala	Pro	Gly	Ile	Gln	Gly	Glu	
				85				90					95			
Lys	Thr	Val	Glu	Gln	Phe	Pro	Gln	Trp	Phe	Gln	Glu	Gln	Gly	Tyr	Lys	
		100					105					110				
Asp	Ile	Pro	Val	Leu	Tyr	Asp	Thr	Lys	Ala	Thr	Thr	Ser	Lys	Leu	Ile	
	115					120						125				
Lys	Phe	Glu	Ala	Phe	Leu	Gln	Asn	Ile								
	130					135										

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1462 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GACTTTTAAC AATAAACTA TTGAAGAGTT GCACAATCTC CTTGTCTCTA AGGAAATTTTC	60
TGCAACAGAA TTGACCCAAG CAACACTTGA AAATATCAAG TCTCGTGAGG AAGCCCTCAA	120
TTCATTTGTC ACCATCGCTG AGGAGCAAGC TCTTGTTCAA GCTAAAGCCA TTGATGAAGC	180
tGGAATTGAT GCTGACAATG TCCTTTTCAGG AATTCCACTT GCTGTTAAGG ATAACATCTC	240
TACAGACGGT ATTCTCACAA CTGCTGCCTC AAAAATGCTC TACAACTATG AGCCAATCTT	300
TGATGCGACa gCTgTTGCCA ATGCAAAAAC CAAGGGCATG ATTGTCGTTG GAAAGACCAA	360
CATGGACGAA TTTGCTATGG GTGGTTCAGG tGAAACTTCA CACTACGGAG CAACTAAAAA	420
CGCTTGGAAC CACAGCAAGG TTCCTGGTGG GTCATCAAGT GGTTCGCGG CAGCTGTAGC	480

09765272.012201

CTCAGGACAA GTTCGCTTGT CACTTGGTTC TGATACTGGT GGTTCATCC GCCAACCTGC 540  
 TGCCTTCAAC GGAATCGTTG GTCTCAAACC AACCTACGGA ACAGTTTCAC GTTTCGGTCT 600  
 CATTGCCTTT GGTAGCTCAT TAGACCAGAT TGGACCTTTT GCTCCTACTG TTAAGGAAAA 660  
 TGCCCTCTTG CTCAACGCTA TTGCCAGCGA AGATGCTAAA GACTCTACTT CTGCTCCTGT 720  
 CCGCATCGCC GACTTTACTT CAAAAATCGG CCAAGACATC AAGGGTATGA AAATCGCTTT 780  
 GCCTAAGGAA TACCTAGGCG AAGGAATTGA TCCAGAGGTT AAGGAAACAA TCTTAAACGC 840  
 GGCCAAACAC TTTGAAAAAT TGGGTGCTAT CGTCGAAGAA GTCAGCCTTC CTCACTCTAA 900  
 ATACGGTGTT GCCGTTTATT ACATCATCGC TTCATCAGAA GCTTCATCAA ACTTGCAACG 960  
 CTTGACGGT ATCCGTTACG GCTATCGCGC AGAAGATGCA ACCAACCTTG ATGAAATCTA 1020  
 TGTAACAGC CGAAGCCAAG GTTTTGGTGA AGAGGTAAAA CGTCGTATCA TGCTGGGTAC 1080  
 TTTCAGTCTT TCATCAGGTT ACTATGATGC CTACTIONAAA AAGGCTGGTC AAGTCCGTAC 1140  
 CCTCATCATT CAAGATTTTCG AAAAAGTCTT CGCGGATTAC GATTTGATTT TGGGTCCAAC 1200  
 TGCTCCAAGT GTTGCCTATG ACTTGATTTC TCTCAACCAT GACCCAGTTG CCATGTACTT 1260  
 AGCCGACCTA TTGACCATAC CTGTAAACTT GGCAGGACTG CCTGGAATTT CGATTCCTGC 1320  
 TGGATTCTCT CAAGGTCTAC CTGTGCGACT CCAATTGATT GGTCCCAAGT ACTCTGAGGA 1380  
 AACCATTTAC CAAGCTGCTG CTGCTTTTGA AGCAACAACA GACTACCACA AACAACAACC 1440  
 CGTGATTTTT GGAGGTGACA AC 1462

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr	Phe	Asn	Asn	Lys	Thr	Ile	Glu	Glu	Leu	His	Asn	Leu	Leu	Val	Ser
1				5					10					15	
Lys	Glu	Ile	Ser	Ala	Thr	Glu	Leu	Thr	Gln	Ala	Thr	Leu	Glu	Asn	Ile
			20					25					30		
Lys	Ser	Arg	Glu	Glu	Ala	Leu	Asn	Ser	Phe	Val	Thr	Ile	Ala	Glu	Glu
		35					40					45			
Gln	Ala	Leu	Val	Gln	Ala	Lys	Ala	Ile	Asp	Glu	Ala	Gly	Ile	Asp	Ala
	50					55					60				
Asp	Asn	Val	Leu	Ser	Gly	Ile	Pro	Leu	Ala	Val	Lys	Asp	Asn	Ile	Ser
65					70					75				80	

09765272-012201

Thr Asp Gly Ile Leu Thr Thr Ala Ala Ser Lys Met Leu Tyr Asn Tyr  
 85 90 95  
 Glu Pro Ile Phe Asp Ala Thr Ala Val Ala Asn Ala Lys Thr Lys Gly  
 100 105 110  
 Met Ile Val Val Gly Lys Thr Asn Met Asp Glu Phe Ala Met Gly Gly  
 115 120 125  
 Ser Gly Glu Thr Ser His Tyr Gly Ala Thr Lys Asn Ala Trp Asn His  
 130 135 140  
 Ser Lys Val Pro Gly Gly Ser Ser Ser Gly Ser Ala Ala Ala Val Ala  
 145 150 155 160  
 Ser Gly Gln Val Arg Leu Ser Leu Gly Ser Asp Thr Gly Gly Ser Ile  
 165 170 175  
 Arg Gln Pro Ala Ala Phe Asn Gly Ile Val Gly Leu Lys Pro Thr Tyr  
 180 185 190  
 Gly Thr Val Ser Arg Phe Gly Leu Ile Ala Phe Gly Ser Ser Leu Asp  
 195 200 205  
 Gln Ile Gly Pro Phe Ala Pro Thr Val Lys Glu Asn Ala Leu Leu Leu  
 210 215 220  
 Asn Ala Ile Ala Ser Glu Asp Ala Lys Asp Ser Thr Ser Ala Pro Val  
 225 230 235 240  
 Arg Ile Ala Asp Phe Thr Ser Lys Ile Gly Gln Asp Ile Lys Gly Met  
 245 250 255  
 Lys Ile Ala Leu Pro Lys Glu Tyr Leu Gly Glu Gly Ile Asp Pro Glu  
 260 265 270  
 Val Lys Glu Thr Ile Leu Asn Ala Ala Lys His Phe Glu Lys Leu Gly  
 275 280 285  
 Ala Ile Val Glu Glu Val Ser Leu Pro His Ser Lys Tyr Gly Val Ala  
 290 295 300  
 Val Tyr Tyr Ile Ile Ala Ser Ser Glu Ala Ser Ser Asn Leu Gln Arg  
 305 310 315 320  
 Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Ala Glu Asp Ala Thr Asn Leu  
 325 330 335  
 Asp Glu Ile Tyr Val Asn Ser Arg Ser Gln Gly Phe Gly Glu Glu Val  
 340 345 350  
 Lys Arg Arg Ile Met Leu Gly Thr Phe Ser Leu Ser Ser Gly Tyr Tyr  
 355 360 365  
 Asp Ala Tyr Tyr Lys Lys Ala Gly Gln Val Arg Thr Leu Ile Ile Gln  
 370 375 380  
 Asp Phe Glu Lys Val Phe Ala Asp Tyr Asp Leu Ile Leu Gly Pro Thr  
 385 390 395 400  
 Ala Pro Ser Val Ala Tyr Asp Leu Asp Ser Leu Asn His Asp Pro Val  
 405 410 415

09765272.012201



Ala Met Tyr Leu Ala Asp Leu Leu Thr Ile Pro Val Asn Leu Ala Gly  
 420 425 430

Leu Pro Gly Ile Ser Ile Pro Ala Gly Phe Ser Gln Gly Leu Pro Val  
 435 440 445

Gly Leu Gln Leu Ile Gly Pro Lys Tyr Ser Glu Glu Thr Ile Tyr Gln  
 450 455 460

Ala Ala Ala Ala Phe Glu Ala Thr Thr Asp Tyr His Lys Gln Gln Pro  
 465 470 475 480

Val Ile Phe Gly Gly Asp Asn  
 485

## (2) INFORMATION FOR SEQ ID NO: 43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTTACAGGT AAACAACCTAC AAGTCGGCGA CAAGGCGCTT GATTTTCTC TTACTACAAC 60

AGATCTTTCT AAAAAATCTC TGGCTGATTT TGATGGCAAG AAAAAAGTCT TGAGTGTCGT 120

TCCTTCTATC GATACAGGCA TCTGCTCAAC TCAAACACGT CGTTTTAATG AAGAATTGGC 180

TGGACTGGAC AACACGGTCG TATTGACTGT TTCAATGGAC CTACCTTTTG CTCAAAAACG 240

TTGGTGCGGT GCTGAAGGCC TTGACAATGC CATTATGCTT TCAGACTACT TTGACCATTG 300

TTTCGGGGCGC GATTATGCCC TCTTGATCAA CGAATGGCAC CTATTAGCAC GCGCAGTCTT 360

TGTCCTCGAT ACTGACAATA CGATTGCTA CGTTGAATAC GTGGATAATA TCAATTCTGA 420

GCCAAACTTC GAA 433

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe Thr Gly Lys Gln Leu Gln Val Gly Asp Lys Ala Leu Asp Phe Ser  
 1 5 10 15

Leu Thr Thr Thr Asp Leu Ser Lys Lys Ser Leu Ala Asp Phe Asp Gly  
 20 25 30

Lys Lys Lys Val Leu Ser Val Val Pro Ser Ile Asp Thr Gly Ile Cys

09765272.012204

35

40

45

Ser Thr Gln Thr Arg Arg Phe Asn Glu Glu Leu Ala Gly Leu Asp Asn  
50 55 60

Thr Val Val Leu Thr Val Ser Met Asp Leu Pro Phe Ala Gln Lys Arg  
65 70 75 80

Trp Cys Gly Ala Glu Gly Leu Asp Asn Ala Ile Met Leu Ser Asp Tyr  
85 90 95

Phe Asp His Ser Phe Gly Arg Asp Tyr Ala Leu Leu Ile Asn Glu Trp  
100 105 110

His Leu Leu Ala Arg Ala Val Phe Val Leu Asp Thr Asp Asn Thr Ile  
115 120 125

Arg Tyr Val Glu Tyr Val Asp Asn Ile Asn Ser Glu Pro Asn Phe Glu  
130 135 140

## (2) INFORMATION FOR SEQ ID NO: 45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

CCAGGCTGAT ACAAGTATCG CAGACATTCA AAAAAGAGGC GAACTGGTTG TCGGTGTCAA      60
ACAAGACGTT CCCAATTTTG GTTACAAAGA TCCAAGACC GGTACTTATT CTGGTATCGA      120
AaCCGACTTG GCCAAGATGG TAGCTGATGA ACTCAAGGTC AAGATTCGCT ATGTGCCGGT      180
TACAGCACAA ACCCGCGGCC CCCTTCTAGA CAATGAACAG GTCGATATGG ATATCGCGAC      240
CTTTACCATC ACGGACGAAC GCAAAAAACT CTACAACTTT ACCAGTCCCT ACTACACAGA      300
CGCTTCTGGA TTTTGGTCA ATAAATCTGC CAAAATCAAA AAGATTGAGG ACCTAAACGG      360
CAAAACCATC GGAGTCGCCC AAGGTTCTAT CACCCAACGC CTGATTACTG AACTGGGTAA      420
AAAGAAAGGT CTGAAGTTTA AATTCGTCGA ACTTGGTTCC TACCCAGAAT TGATTACTTC      480
CCTGCACGCT CATCGTATCG ATACCTTTTC CGTTGACCGC TCTATTCTAT CTGGCTACAC      540
TAGTAAACGG ACAGCACTAC TAGATGATAG TTTCAAGCCA TCTGACTACG GTATTGTTAC      600
CAAGAAATCA AATACAGAGC TCAACGACTA TCTTGATAAC TTGGTTACTA AATGGAGCAA      660
GGATGGTAGT TTGCAGAAAC TTTATGACCG TTACAAGCTC AAACCATCTA GCCATACTGC      720
AGAT                                          724

```

## (2) INFORMATION FOR SEQ ID NO: 46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid

09765272.012201

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gln Ala Asp Thr Ser Ile Ala Asp Ile Gln Lys Arg Gly Glu Leu Val  
 1 5 10 15  
 Val Gly Val Lys Gln Asp Val Pro Asn Phe Gly Tyr Xaa Asp Pro Lys  
 20 25 30  
 Thr Gly Thr Tyr Ser Gly Ile Glu Thr Asp Leu Ala Lys Met Val Ala  
 35 40 45  
 Asp Glu Leu Lys Val Lys Ile Arg Tyr Val Pro Val Thr Ala Gln Thr  
 50 55 60  
 Arg Gly Pro Leu Leu Asp Asn Glu Gln Val Asp Met Asp Ile Ala Thr  
 65 70 75 80  
 Phe Thr Ile Thr Asp Glu Arg Lys Lys Leu Tyr Asn Phe Thr Ser Pro  
 85 90 95  
 Tyr Tyr Thr Asp Ala Ser Gly Phe Leu Val Asn Lys Ser Ala Lys Ile  
 100 105 110  
 Lys Lys Ile Glu Asp Leu Asn Gly Lys Thr Ile Gly Val Ala Gln Gly  
 115 120 125  
 Ser Ile Thr Gln Arg Leu Ile Thr Glu Leu Gly Lys Lys Lys Gly Leu  
 130 135 140  
 Lys Phe Lys Phe Val Glu Leu Gly Ser Tyr Pro Glu Leu Ile Thr Ser  
 145 150 155 160  
 Leu His Ala His Arg Ile Asp Thr Phe Ser Val Asp Arg Ser Ile Leu  
 165 170 175  
 Ser Gly Tyr Thr Ser Lys Arg Thr Ala Leu Leu Asp Asp Ser Phe Lys  
 180 185 190  
 Pro Ser Asp Tyr Gly Ile Val Thr Lys Lys Ser Asn Thr Glu Leu Asn  
 195 200 205  
 Asp Tyr Leu Asp Asn Leu Val Thr Lys Trp Ser Lys Asp Gly Ser Leu  
 210 215 220  
 Gln Lys Leu Tyr Asp Arg Tyr Lys Leu Lys Pro Ser Ser His Thr Ala  
 225 230 235 240  
 Asp

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

09765272.012201

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTCTGTATCA TTTGAAAACA AAGAAACAAA CCGTGGTGTG TTgACTTTCA CTATCTCTCA 60  
 AGACCAAATC AAACCAGAAT TGGACCGTGT CTTCAAGtCA GTGAAGAAAT CTCTTAATGT 120  
 TCCAGGTTTC CGTAAAGGTC ACCTTCCACG CCCTATCTTC GACCAAAAAT TTGGTGAAGA 180  
 AGCTCTTTAT CAAGATGCAA TGAACGCACT TTTGCCAAAC GCTTATGAAG CAGCTGTAAA 240  
 AGAAGCTGGT CTTGAAGTGG TTGCCCAACC AAAAATTGAC GTAACCTCAA TGGAAAAAGG 300  
 TCAAGACTGG GTTATCACTG CTGAAGTCGT TACAAAACCT GAAGTAAAAT TGGGTGACTA 360  
 CAAAAACCTT GAAGTATCAG TTGATGTAGA AAAAGAAGTA ACTGACGCTG ATGTCTGAAGA 420  
 GCGTATCGAA CGCGAACGCA ACAACCTGGC TGAATTGGTT ATCAAGGAAG CTGCTGCTGA 480  
 AAACGGCGAC ACTGTTGTGA TCGACTTCGT TGGTTCATC GACGGTGTTG AATTTGACGG 540  
 TGGAAAAGGT GAAAACCTCT CACTTGGACT TGGTTCAGGT CAATTCATCC CTGGTTTCGA 600  
 AGACCAATTG GTAGGTCAC T CAGCTGGCGA AACCGTTGAT GTTATCGTAA CATTCCCAGA 660  
 AGACTACCAA GCAGAAGACC TTGCAGGTAA AGAAGCTAAA TTCGTGACAA CTATCCACGA 720  
 AGTAAAAGCT AAAGAAGTTC CGGCTCTTGA CGATGAACTT GCAAAAGACA TTGATGAAGA 780  
 AGTTGAAACA CTTGCTGACT TGAAAGAAAA ATACAGCAAA GAATTGGCTG CTGCTAAAGA 840  
 AGAAGCTTAC AAAGATGCAG TTGAAGGTGC AGCAATTGAT ACAGCTGTAG AAAATGCTGA 900  
 AATCGTAGAA CTTCCAGAAG AAATGATCCA TGAAGAAGTT CACCGTTCAG TAAATGAATT 960  
 CCTTGGAAT TTGCAACGTC AAGGGATCAA CCCTGACATG TACTTCCAAA TCACTGGAAC 1020  
 TACTCAAGAA GACCTTCACA ACCAATACCA AGCAGAAGCT GAGTCACGTA CTAAGACTAA 1080  
 CCTTGTTATC GAAGCAGTTG CCAAAGCTGA AGGATTTGAT GCTTCAGAAG AAGAAATCCA 1140  
 AAAAGAAGTT GAGCAATTGG CAGCAGACTA CAACATGGAA GTTGCACAAG TTCAAAACTT 1200  
 GCTTTCAGCT GACATGTTGA AACATGATAT CACTATCAAA AAAGCTGTTG AATTGATCAC 1260  
 AAGCACAGCA ACAGTAAAA 1279

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Val Ser Phe Glu Asn Lys Glu Thr Asn Arg Gly Val Leu Thr Phe

09765272.012201

1	5	10	15												
Thr	Ile	Ser	Gln	Asp	Gln	Ile	Lys	Pro	Glu	Leu	Asp	Arg	Val	Phe	Lys
			20					25						30	
Ser	Val	Lys	Lys	Ser	Leu	Asn	Val	Pro	Gly	Phe	Arg	Lys	Gly	His	Leu
		35					40					45			
Pro	Arg	Pro	Ile	Phe	Asp	Gln	Lys	Phe	Gly	Glu	Glu	Ala	Leu	Tyr	Gln
	50					55					60				
Asp	Ala	Met	Asn	Ala	Leu	Leu	Pro	Asn	Ala	Tyr	Glu	Ala	Ala	Val	Lys
65					70					75					80
Glu	Ala	Gly	Leu	Glu	Val	Val	Ala	Gln	Pro	Lys	Ile	Asp	Val	Thr	Ser
				85					90					95	
Met	Glu	Lys	Gly	Gln	Asp	Trp	Val	Ile	Thr	Ala	Glu	Val	Val	Thr	Lys
			100					105						110	
Pro	Glu	Val	Lys	Leu	Gly	Asp	Tyr	Lys	Asn	Leu	Glu	Val	Ser	Val	Asp
			115				120						125		
Val	Glu	Lys	Glu	Val	Thr	Asp	Ala	Asp	Val	Glu	Glu	Arg	Ile	Glu	Arg
	130					135						140			
Glu	Arg	Asn	Asn	Leu	Ala	Glu	Leu	Val	Ile	Lys	Glu	Ala	Ala	Ala	Glu
145					150					155					160
Asn	Gly	Asp	Thr	Val	Val	Ile	Asp	Phe	Val	Gly	Ser	Ile	Asp	Gly	Val
				165					170					175	
Glu	Phe	Asp	Gly	Gly	Lys	Gly	Glu	Asn	Phe	Ser	Leu	Gly	Leu	Gly	Ser
			180					185					190		
Gly	Gln	Phe	Ile	Pro	Gly	Phe	Glu	Asp	Gln	Leu	Val	Gly	His	Ser	Ala
		195					200					205			
Gly	Glu	Thr	Val	Asp	Val	Ile	Val	Thr	Phe	Pro	Glu	Asp	Tyr	Gln	Ala
	210					215					220				
Glu	Asp	Leu	Ala	Gly	Lys	Glu	Ala	Lys	Phe	Val	Thr	Thr	Ile	His	Glu
225					230					235					240
Val	Lys	Ala	Lys	Glu	Val	Pro	Ala	Leu	Asp	Asp	Glu	Leu	Ala	Lys	Asp
				245					250					255	
Ile	Asp	Glu	Glu	Val	Glu	Thr	Leu	Ala	Asp	Leu	Lys	Glu	Lys	Tyr	Ser
			260					265					270		
Lys	Glu	Leu	Ala	Ala	Ala	Lys	Glu	Glu	Ala	Tyr	Lys	Asp	Ala	Val	Glu
		275					280					285			
Gly	Ala	Ala	Ile	Asp	Thr	Ala	Val	Glu	Asn	Ala	Glu	Ile	Val	Glu	Leu
	290					295					300				
Pro	Glu	Glu	Met	Ile	His	Glu	Glu	Val	His	Arg	Ser	Val	Asn	Glu	Phe
305					310					315					320
Leu	Gly	Asn	Leu	Gln	Arg	Gln	Gly	Ile	Asn	Pro	Asp	Met	Tyr	Phe	Gln
				325					330					335	
Ile	Thr	Gly	Thr	Thr	Gln	Glu	Asp	Leu	His	Asn	Gln	Tyr	Gln	Ala	Glu

09765272-012201

159

340

345

350

Ala Glu Ser Arg Thr Lys Thr Asn Leu Val Ile Glu Ala Val Ala Lys  
355 360 365

Ala Glu Gly Phe Asp Ala Ser Glu Glu Glu Ile Gln Lys Glu Val Glu  
370 375 380

Gln Leu Ala Ala Asp Tyr Asn Met Glu Val Ala Gln Val Gln Asn Leu  
385 390 395 400

Leu Ser Ala Asp Met Leu Lys His Asp Ile Thr Ile Lys Lys Ala Val  
405 410 415

Glu Leu Ile Thr Ser Thr Ala Thr Val Lys  
420 425

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

TGGTCAAAAG GAAAGTCAGA CAGGAAAGGG GATGAAAATT GTGACCAGTT TTTATCCTAT	60
CTACGCTATG GTTAAGGAAG TATCTGGTGA CTTGAATGAT GTTCGGATGA TTCAGTCAAG	120
TAGTGGTATT CACTCCTTTG AACCTTCGGC AAATGATATC GCAGCCATCT ATGATGCAGA	180
TGTCTTTGTT TACCATTCTC ATACACTCGA ATCTTGGGCA GGAAGTCTGG ATCCAAATCT	240
AAAAAATCC AAAGTGAAGG TCTTAGAGGC TTCTGAGGGA ATGACCTTGG AACGTGTCCC	300
TGGACTAGAG GATGTGGAAG CAGGGGATGG AGTTGATGAA AAAACGCTCT ATGACCCTCA	360
CACATGGCTA GATCCTGAAA AAGCTGGAGA AGAAGCCCAA ATTATCGCTG ATAAACTTTC	420
AGAGGTGGAT AGTGAGCATA AAGAGACTTA TCAAAAAAAT GCGCAACCTT TATCAAAAAA	480
GCTCAGGAAT	490

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Gln Lys Glu Ser Gln Thr Gly Lys Gly Met Lys Ile Val Thr Ser
1 5 10 15

09765272 012201

Phe Tyr Pro Ile Tyr Ala Met Val Lys Glu Val Ser Gly Asp Leu Asn  
 20 25 30  
 Asp Val Arg Met Ile Gln Ser Ser Ser Gly Ile His Ser Phe Glu Pro  
 35 40 45  
 Ser Ala Asn Asp Ile Ala Ala Ile Tyr Asp Ala Asp Val Phe Val Tyr  
 50 55 60  
 His Ser His Thr Leu Glu Ser Trp Ala Gly Ser Leu Asp Pro Asn Leu  
 65 70 75 80  
 Lys Lys Ser Lys Val Lys Val Leu Glu Ala Ser Glu Gly Met Thr Leu  
 85 90 95  
 Glu Arg Val Pro Gly Leu Glu Asp Val Glu Ala Gly Asp Gly Val Asp  
 100 105 110  
 Glu Lys Thr Leu Tyr Asp Pro His Thr Trp Leu Asp Pro Glu Lys Ala  
 115 120 125  
 Gly Glu Glu Ala Gln Ile Ile Ala Asp Lys Leu Ser Glu Val Asp Ser  
 130 135 140  
 Glu His Lys Glu Thr Tyr Gln Lys Asn Ala Gln Pro Leu Ser Lys Lys  
 145 150 155 160  
 Leu Arg Asn

## (2) INFORMATION FOR SEQ ID NO: 51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GAAGGATAGA TATATTTTAG CATTTGAGAC ATCCTGTGAT GAGACCAGTG TCGCCGTCTT 60  
 GAAAAACGAC GATGAGCTCT TGTCCAATGT CATTGCTAGT CAAATTGAGA GTCACAAACG 120  
 TTTTGGTGGC GTAGTGCCCG AAGTAGCCAG TCGTCACCAT GTCGAGGTCA TTACAGCCTG 180  
 TATCGAGGAG GCATTGGCAG AAGCAGGGAT TACCGAAGAG GACGTGACAG CTGTTGCGGT 240  
 TACCTACGGA CCAGGCTTGG TCGGAGCCTT GCTAGTTGGT TTGTCAGCTG CCAAGGCCTT 300  
 TGCTTGGGCT CACGGACTTC CACTGATTCC TGTTAATCAC ATGGCTGGGC ACCTCATGGC 360  
 AGCTCAGAGT GTGGAGCCTT TGGAGTTTCC CTTGCTAGCC CTCTTGGTCA GCGGCGGACA 420  
 CACAGAGTTG GTTTATGTTT CGGAGGCAGG AGATTATAAG ATTGTTGGGG AAACCCGTGA 480  
 TGATGCGGTT GGTGAGGCTT ATGATAAGGT CGGCCGTGTC ATGGGCTTGA CCTATCCTGC 540  
 AGGTCGTGAG ATTGACGAGC TGGCTCATCA GGGGCAGGAT ATTTATGATT TCCCCCGTGC 600  
 CATGATTAAG GAAGATAATC TGGAGTTCTC CTTCTCAGGT TTGAAATCTG CCTTTATCAA 660

TCTTCATCAC AATGCCGAGC AAAAGGGAGA AAGCCTGTCT ACAGAAGATT TGTGTGCTTC 720  
 CTTCCAAGCA GCAGTTATGG ACATTCTCAT GGCAAAAACC AAGAAGGCTT TGGAGAAATA 780  
 TCCTGTAAAA ATCCTAGTTG TGGCAGGTGG TGTGGCAGCC AATAAAGGTC TCAGAGAACG 840  
 CCTAGCAGCC GAAATCACAG ATGTCAAGGT TATCATCCCC CCTCTGCGAC TCTGCGGAGA 900  
 CAATGCAGGT ATGATTGCCT ATGCCAGCGT CAGCNAGTGG AACAAAGAAA ACTTCGCAGG 960  
 CTGGGACCTC AATGCCAAAC CAAGTCTTGC CTTTGATACC ATGGAA 1006

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Lys Asp Arg Tyr Ile Leu Ala Phe Glu Thr Ser Cys Asp Glu Thr Ser  
 1 5 10 15  
 Val Ala Val Leu Lys Asn Asp Asp Glu Leu Leu Ser Asn Val Ile Ala  
 20 25 30  
 Ser Gln Ile Glu Ser His Lys Arg Phe Gly Gly Val Val Pro Glu Val  
 35 40 45  
 Ala Ser Arg His His Val Glu Val Ile Thr Ala Cys Ile Glu Glu Ala  
 50 55 60  
 Leu Ala Glu Ala Gly Ile Thr Glu Glu Asp Val Thr Ala Val Ala Val  
 65 70 75 80  
 Thr Tyr Gly Pro Gly Leu Val Gly Ala Leu Leu Val Gly Leu Ser Ala  
 85 90 95  
 Ala Lys Ala Phe Ala Trp Ala His Gly Leu Pro Leu Ile Pro Val Asn  
 100 105 110  
 His Met Ala Gly His Leu Met Ala Ala Gln Ser Val Glu Pro Leu Glu  
 115 120 125  
 Phe Pro Leu Leu Ala Leu Leu Val Ser Gly Gly His Thr Glu Leu Val  
 130 135 140  
 Tyr Val Ser Glu Ala Gly Asp Tyr Lys Ile Val Gly Glu Thr Arg Asp  
 145 150 155 160  
 Asp Ala Val Gly Glu Ala Tyr Asp Lys Val Gly Arg Val Met Gly Leu  
 165 170 175  
 Thr Tyr Pro Ala Gly Arg Glu Ile Asp Glu Leu Ala His Gln Gly Gln  
 180 185 190  
 Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile Lys Glu Asp Asn Leu Glu

09765272.012201



195	200	205
Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe Ile Asn Leu His His Asn		
210	215	220
Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr Glu Asp Leu Cys Ala Ser		
225	230	235 240
Phe Gln Ala Ala Val Met Asp Ile Leu Met Ala Lys Thr Lys Lys Ala		
245	250	255
Leu Glu Lys Tyr Pro Val Lys Ile Leu Val Val Ala Gly Gly Val Ala		
260	265	270
Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala Ala Glu Ile Thr Asp Val		
275	280	285
Lys Val Ile Ile Pro Pro Leu Arg Leu Cys Gly Asp Asn Ala Gly Met		
290	295	300
Ile Ala Tyr Ala Ser Val Ser Xaa Trp Asn Lys Glu Asn Phe Ala Gly		
305	310	315 320
Trp Asp Leu Asn Ala Lys Pro Ser Leu Ala Phe Asp Thr Met Glu		
325	330	335

## (2) INFORMATION FOR SEQ ID NO: 53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGTAGTTAAA GTTGGTATTA ACGGTTTCGG ACGTATCGGT CGTCTTGCTT TCCGTCGTAT	60
CCAAAACGTA GAAGGTGTTG AAGTTACACG CATCAACGAC CTTACAGATC CAGTTATGCT	120
TGCACACTTG TTGAAATACG ACACAACTCA AGGTCGTTTC GACGGTACTG TTGAAGTTAA	180
AGAAGGTGGA TTTGAAGTTA ACGGTAAATT CATCAAAGTT TCTGCTGAAC GTGATCCAGA	240
ACAAATCGAC TGGGCTACTG ACGGTGTAGA AATCGTTCTT GAAGCTACTG GTTTCTTTGC	300
TAAGAAAGAA GCAGCTGAAA AACACCTTAA AGGTGGAGCT AAAAAAGTTG TTATCACTGC	360
TCCTGGTGGA AACGACGTTA AAACAGTTGT ATTCAACACT AACCACGACG TTCTTGACGG	420
TACTGAAACA GTTATCTCAG GTGCTTCATG TACTACAAAC TGCTTGGCTC CAATGGCTAA	480
AGCTCTTCAA GACAACTTTG GTGTTGTTGA AGGATTGATG ACTACTATCC ACGCTTACAC	540
TGGTGACCAA ATGATCCTTG ACGGACCACA CCGTGGTGGT GACCTTCGCC GTGCTCGCGC	600
TGGTGCTGCA AACATCGTTC CTA ACTCAAC TGGTGCTGCA AAAGCTATCG GTCTTGTAAT	660
CCCAGAATTG AATGGTAAAC TTGACGGATC TGCACAACGC GTTCCAAC TC CAACTGGATC	720
AGTTACTGAA TTGGTAGCAG TTCTTGAAAA GAACGTTACT GTTGATGAAG TGAACGCAGC	780

09765272.012201

TATGAAAGCA GCTTCAAACG AATCATACGG TTACACAGAA GATCCAATCG TATCTTCAGA 840  
 TATCGTAGGT ATGTCTTACG GTTCATTGTT TGACGCAACT CAACTAAAG TTCTTGACGT 900  
 TGACGGTAAA CAATTGGTTA AAGTTGTATC ATGGTACGAC AACGAAATGT CATACTGTC 960  
 ACAACTTGTT CGTACTCTTG GAATACTTCG CAAAAATTGC 1000

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala  
 1 5 10 15  
 Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn  
 20 25 30  
 Asp Leu Thr Asp Pro Val Met Leu Ala His Leu Leu Lys Tyr Asp Thr  
 35 40 45  
 Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe  
 50 55 60  
 Glu Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu  
 65 70 75 80  
 Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Thr  
 85 90 95  
 Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu Lys Gly Gly  
 100 105 110  
 Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val Lys Thr  
 115 120 125  
 Val Val Phe Asn Thr Asn His Asp Val Leu Asp Gly Thr Glu Thr Val  
 130 135 140  
 Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys  
 145 150 155 160  
 Ala Leu Gln Asp Asn Phe Gly Val Val Glu Gly Leu Met Thr Thr Ile  
 165 170 175  
 His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His Arg Gly  
 180 185 190  
 Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val Pro Asn  
 195 200 205  
 Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu Leu Asn  
 210 215 220

09765272.012204

Gly Lys Leu Asp Gly Ser Ala Gln Arg Val Pro Thr Pro Thr Gly Ser  
225 230 235 240

Val Thr Glu Leu Val Ala Val Leu Glu Lys Asn Val Thr Val Asp Glu  
245 250 255

Val Asn Ala Ala Met Lys Ala Ala Ser Asn Glu Ser Tyr Gly Tyr Thr  
260 265 270

Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Tyr Gly Ser  
275 280 285

Leu Phe Asp Ala Thr Gln Thr Lys Val Leu Asp Val Asp Gly Lys Gln  
290 295 300

Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr Thr Ala  
305 310 315 320

Gln Leu Val Arg Thr Leu Gly Ile Leu Arg Lys Asn Cys  
325 330

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TTCTTACGAG TTGGGACTGT ATCAAGCTAG AACGGTTAAG GAAAATAATC GTGTTTCCTA	60
TATAGATGGA AAACAAGCGA CGCAAAAAC GGAGAATTTG ACTCCTGATG AGGTTAGCAA	120
GCGTGAAGGA ATCAATGCTG AGCAAATCGT CATCAAGATA ACAGACCAAG GCTATGTCAC	180
TTCACATGGC GACCACTATC ATTATTACAA TGGTAAGGTT CCTTATGACG CTATCATCAG	240
TGAAGAATTA CTCATGAAAG ATCCAAACTA TAAGCTAAAA GATGAGGATA TTGTTAATGA	300
GGTCAAGGGT GGATATGTTA TCAAGGTAGA TGGAAAATAC TATGTTTACC TTAAGGATGC	360
TGCCCACGCG GATAACGTCC GTACAAAAGA GGAAATCAAT CGACAAAAC AAGAGCATAG	420
TCAACATCGT GAAGGTGGAA CTCCAAGAAA CGATGGTGCT GTTGCCTTGG CACGTTTCGCA	480
AGGACGCTAT ACTACAGATG ATGGTTATAT CTTTAATGCT TCTGATATCA TAGAGGATAC	540
TGGTGATGCT TATATCGTTC CTCATGGAGA TCATTACCAT TACATTCCCTA AGAATGAGTT	600
ATCAGCTAGC GAGTTGGCTG CTGCAGAAGC CTTCTATCT GGTGAGGAA ATCTGTCAAA	660
TTCAAGAACC TATCGCCGAC AAAATAGCGA TAACACTTCA AGAACAAACT GGGTACCTTC	720
TGTAAGCAAT CCAGGAATA CAAATACTAA CACAAGCAAC AACAGCAACA CTAACAGTCA	780
AGCAAGTCAA AGTAATGACA TTGATAGTCT CTTGAAACAG CTCTACAAAC TGCCTTTGAG	840
TCAACGACAT GTAGAATCTG ATGGCCTTGT CTTTGATCCA GCACAAATCA CAAGTCGAAC	900
AGCTAGAGGT GTTGCAGTGC CACACGGAGA TCATTACCAC TTCATCCCTT ACTCTCAAAT	960

09765272.012201

GTCTGAATTG GAAGAACGAA TCGCTCGTAT TATTCCCCTT CGTTATCGTT CAAACCATTG 1020  
 GGTACCAGAT TCAAGGCCAG AACAAACCAAG TCCACAACCG ACTCCGGAAC CTAGTCCAGG 1080  
 CCCGCAACCT GCACCAAATC TTAAATAGA CTCAAATTCT TCTTTGGTTA GTCAGCTGGT 1140  
 ACGAAAAGTT GGGGAAGGAT ATGTATTCTGA AGAAAAGGGC ATCTCTCGTT ATGTCTTTGC 1200  
 GAAAGATTTA CCATCTGAAA CTGTTAAAAA TCTTGAAAGC AAGTTATCAA AACAAAGAGAG 1260  
 TGTTTCACAC ACTTTAACTG CTAAAAAGA AAATGTTGCT CCTCGTGACC AAGAATTTTA 1320  
 TGATAAAGCA TATAATCTGT TAACTGAGGC TCATAAGCC TTGTTTGNAA ATAAGGGTCG 1380  
 TAATTCTGAT TTCCAAGCCT TAGACAAATT ATTAGAACGC TTGAATGATG AATCGACTAA 1440  
 TAAAGAAAAA TTGGTAGATG ATTTATTGGC ATTCTAGCA CCAATTACCC ATCCAGAGCG 1500  
 ACTTGGCAA CCAAATTCTC AAATTGAGTA TACTGAAGAC GAAGTTCGTA TTGCTCAATT 1560  
 AGCTGATAAG TATACAACGT CAGATGGTTA CATTTTTGAT GAACATGATA TAATCAGTGA 1620  
 TGAAGGAGAT GCATATGTAA CGCCTCATAT GGGCCATAGT CACTGGATTG GAAAAGATAG 1680  
 CCTTTCTGAT AAGGAAAAAG TTGCAGCTCA AGCCTATACT AAAGAAAAAG GTATCCTACC 1740  
 TCCATCTCCA GACGCAGATG TTAAAGCAA TCCAACTGGA GATAGTGCAG CAGCTATTTA 1800  
 CAATCGTGTG AAAGGGGAAA AACGAATTCC ACTCGTTCGA CTTCCATATA TGGTTGAGCA 1860  
 TACAGTTGAG GTTAAAAACG GTAATTTGAT TATTCCTCAT AAGGATCATT ACCATAATAT 1920  
 TAAATTTGCT TGGTTTGATG ATCACACATA CAAAGCTCCA AATGGCTATA CCTTGGAAGA 1980  
 TTTGTTTGGC ACGATTAAGT ACTACGTAGA ACACCCTGAC GAACGTCCAC ATTCTAATGA 2040  
 TGGATGGGGC AATGCCAGTG AGCATGTGTT AGGCAAGAAA GACCACAGTG AAGATCCAAA 2100  
 TAAGAACTTC AAAGCGGATG AAGAGCCAGT AGAGGAAACA CCTGCTGAGC CAGAAGTCCC 2160  
 TCAAGTAGAG ACTGAAAAAG TAGAAGCCCA ACTCAAAGAA GCAGAAGTTT TGCTTGCGAA 2220  
 AGTAACGGAT TCTAGTCTGA AAGCCAATGC AACAGAACT CTAGCTGGTT TACGAAATAA 2280  
 TTTGACTCTT CAAATTATGG ATAACAATAG TATCATGGCA GAAGCAGAAA AATTACTTGC 2340  
 GTTGTTAAAA GGAAGTAATC CTTCATCTGT AAGTAAGGAA AAAATAAAC 2389

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Tyr Glu Leu Gly Leu Tyr Gln Ala Arg Thr Val Lys Glu Asn Asn

09765272.012201

1	5	10	15
Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln Lys Thr Glu Asn	20	25	30
Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala Glu Gln	35	40	45
Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp	50	55	60
His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile Ile Ser	65	70	75
Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Lys Leu Lys Asp Glu Asp	85	90	95
Ile Val Asn Glu Val Lys Gly Gly Tyr Val Ile Lys Val Asp Gly Lys	100	105	110
Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr	115	120	125
Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu His Ser Gln His Arg Glu	130	135	140
Gly Gly Thr Pro Arg Asn Asp Gly Ala Val Ala Leu Ala Arg Ser Gln	145	150	155
Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile	165	170	175
Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr	180	185	190
His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala Ala	195	200	205
Glu Ala Phe Leu Ser Gly Arg Gly Asn Leu Ser Asn Ser Arg Thr Tyr	210	215	220
Arg Arg Gln Asn Ser Asp Asn Thr Ser Arg Thr Asn Trp Val Pro Ser	225	230	235
Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser Asn Asn Ser Asn	245	250	255
Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp Ser Leu Leu Lys	260	265	270
Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val Glu Ser Asp Gly	275	280	285
Leu Val Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala Arg Gly Val	290	295	300
Ala Val Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Gln Met	305	310	315
Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile Ile Pro Leu Arg Tyr Arg	325	330	335
Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro Ser Pro Gln			

09765272.012201

340

345

350

Pro Thr Pro Glu Pro Ser Pro Gly Pro Gln Pro Ala Pro Asn Leu Lys  
 355 360 365  
 Ile Asp Ser Asn Ser Ser Leu Val Ser Gln Leu Val Arg Lys Val Gly  
 370 375 380  
 Glu Gly Tyr Val Phe Glu Glu Lys Gly Ile Ser Arg Tyr Val Phe Ala  
 385 390 395 400  
 Lys Asp Leu Pro Ser Glu Thr Val Lys Asn Leu Glu Ser Lys Leu Ser  
 405 410 415  
 Lys Gln Glu Ser Val Ser His Thr Leu Thr Ala Lys Lys Glu Asn Val  
 420 425 430  
 Ala Pro Arg Asp Gln Glu Phe Tyr Asp Lys Ala Tyr Asn Leu Leu Thr  
 435 440 445  
 Glu Ala His Lys Ala Leu Phe Xaa Asn Lys Gly Arg Asn Ser Asp Phe  
 450 455 460  
 Gln Ala Leu Asp Lys Leu Leu Glu Arg Leu Asn Asp Glu Ser Thr Asn  
 465 470 475 480  
 Lys Glu Lys Leu Val Asp Asp Leu Leu Ala Phe Leu Ala Pro Ile Thr  
 485 490 495  
 His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile Glu Tyr Thr Glu  
 500 505 510  
 Asp Glu Val Arg Ile Ala Gln Leu Ala Asp Lys Tyr Thr Thr Ser Asp  
 515 520 525  
 Gly Tyr Ile Phe Asp Glu His Asp Ile Ile Ser Asp Glu Gly Asp Ala  
 530 535 540  
 Tyr Val Thr Pro His Met Gly His Ser His Trp Ile Gly Lys Asp Ser  
 545 550 555 560  
 Leu Ser Asp Lys Glu Lys Val Ala Ala Gln Ala Tyr Thr Lys Glu Lys  
 565 570 575  
 Gly Ile Leu Pro Pro Ser Pro Asp Ala Asp Val Lys Ala Asn Pro Thr  
 580 585 590  
 Gly Asp Ser Ala Ala Ala Ile Tyr Asn Arg Val Lys Gly Glu Lys Arg  
 595 600 605  
 Ile Pro Leu Val Arg Leu Pro Tyr Met Val Glu His Thr Val Glu Val  
 610 615 620  
 Lys Asn Gly Asn Leu Ile Ile Pro His Lys Asp His Tyr His Asn Ile  
 625 630 635 640  
 Lys Phe Ala Trp Phe Asp Asp His Thr Tyr Lys Ala Pro Asn Gly Tyr  
 645 650 655  
 Thr Leu Glu Asp Leu Phe Ala Thr Ile Lys Tyr Tyr Val Glu His Pro  
 660 665 670  
 Asp Glu Arg Pro His Ser Asn Asp Gly Trp Gly Asn Ala Ser Glu His

09765272.012201

675

680

685

Val Leu Gly Lys Lys Asp His Ser Glu Asp Pro Asn Lys Asn Phe Lys  
690 695 700

Ala Asp Glu Glu Pro Val Glu Glu Thr Pro Ala Glu Pro Glu Val Pro  
705 710 715 720

Gln Val Glu Thr Glu Lys Val Glu Ala Gln Leu Lys Glu Ala Glu Val  
725 730 735

Leu Leu Ala Lys Val Thr Asp Ser Ser Leu Lys Ala Asn Ala Thr Glu  
740 745 750

Thr Leu Ala Gly Leu Arg Asn Asn Leu Thr Leu Gln Ile Met Asp Asn  
755 760 765

Asn Ser Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu Leu Lys Gly  
770 775 780

Ser Asn Pro Ser Ser Val Ser Lys Glu Lys Ile Asn  
785 790 795

## (2) INFORMATION FOR SEQ ID NO: 57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TACTGAGATG CATCATAATC TAGGAGCTGA AAAGCGTTCA GCAGTGGCTA CTACTATCGA	60
TAGTTTTAAG GAGCGAAGTC AAAAAGTCAG AGCACTATCT GATCCAAATG TGCGTTTTGT	120
TCCCTTCTTT GGCTCTAGTG AATGGCTTCG TTTTGACGGT GCTCATTCTG CGGTATTAGC	180
TGAGAAATAC AATCGTTCCT ACCGTCCTTA TCTTTTAGGA CAGGGGGGAG CTGCATCGCT	240
TAACCAATAT TTTGGAATGC AACAGATGTT ACCACAGCTG GAGAATAAAC AAGTTGTGTA	300
TGTTATCTCA CCTCAGTGGT TCAGTAAAAA TGGCTATGAT CCAGCAGCCT TCCAGCAGTA	360
TTTTAATGGA GACCAATTGA CTAGTTTTCT GAAACATCAA TCTGGGGATC AGGCTAGTCA	420
ATATGCAGCG ACTCGCTTAC TGCAACAGTT CCCAAACGTA GCTATGAAGG ACCTGGTTCA	480
GAAGTTGGCA AGTAAAGAAG AATTGTCGAC AGCAGACAAT GAAATGATTG AATTATTGGC	540
TCGTTTTAAT GAACGCCAAG CTCCTTTTTT TGGTCAGTTT TCGGTTAGAG GCTATGTTAA	600
CTACGATAAG CATGTAGCTA AGTATTTAAA AATCTTGCCA GACCAGTTTT CTTATCAGGC	660
AATAGAAGAT GTTGTCAAAG CAGATGCTGA AAAAAATACT TCCAATAATG AGATGGGAAT	720
GGAAAATTAT TTCTATAATG AGCAGATCAA GAAGGATTTG AAGAAATTAA AGGATTCTCA	780
GAAAAGCTTT ACCTATCTCA AGTCGCCAGA GTATAATGNN TTGCAGTTGG TTTTAACACA	840

09765272.012201

GTTTTCTAAA TCTAAGGTAA ACCCGATTTT TATCATTCCA CCTGTTAATA AAAAATGGAT 900  
 GNACTATGCT GGTCTACGAG AGGATATGTA CCAACAAACG GTGCAGAAGA TTCGCTACCA 960  
 GTTAGAAAGT CAAGGTTTTA CCAATATAGC AGATTTTTCT AAGGACGGCG GGGAGCCTTT 1020  
 CTTTATGAAG GACACCATTC ACCTTGTTG GTTGGGTTGG TTGGCTTTTG ACAAGGCAGT 1080  
 TGATCCTTTC CTATCCAATC CCACACCAGC TCCGACTTAC CATCTGAATG AGCGCTTTTT 1140  
 CAGCAAAGAT TGGGCGACTT ATGATGGAGA TGTCAAAGAA 1180

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Thr	Glu	Met	His	His	Asn	Leu	Gly	Ala	Glu	Lys	Arg	Ser	Ala	Val	Ala	1	5	10	15
Thr	Thr	Ile	Asp	Ser	Phe	Lys	Glu	Arg	Ser	Gln	Lys	Val	Arg	Ala	Leu	20	25	30	
Ser	Asp	Pro	Asn	Val	Arg	Phe	Val	Pro	Phe	Phe	Gly	Ser	Ser	Glu	Trp	35	40	45	
Leu	Arg	Phe	Asp	Gly	Ala	His	Ser	Ala	Val	Leu	Ala	Glu	Lys	Tyr	Asn	50	55	60	
Arg	Ser	Tyr	Arg	Pro	Tyr	Leu	Leu	Gly	Gln	Gly	Gly	Ala	Ala	Ser	Leu	65	70	75	80
Asn	Gln	Tyr	Phe	Gly	Met	Gln	Gln	Met	Leu	Pro	Gln	Leu	Glu	Asn	Lys	85	90	95	
Gln	Val	Val	Tyr	Val	Ile	Ser	Pro	Gln	Trp	Phe	Ser	Lys	Asn	Gly	Tyr	100	105	110	
Asp	Pro	Ala	Ala	Phe	Gln	Gln	Tyr	Phe	Asn	Gly	Asp	Gln	Leu	Thr	Ser	115	120	125	
Phe	Leu	Lys	His	Gln	Ser	Gly	Asp	Gln	Ala	Ser	Gln	Tyr	Ala	Ala	Thr	130	135	140	
Arg	Leu	Leu	Gln	Gln	Phe	Pro	Asn	Val	Ala	Met	Lys	Asp	Leu	Val	Gln	145	150	155	160
Lys	Leu	Ala	Ser	Lys	Glu	Glu	Leu	Ser	Thr	Ala	Asp	Asn	Glu	Met	Ile	165	170	175	
Glu	Leu	Leu	Ala	Arg	Phe	Asn	Glu	Arg	Gln	Ala	Ser	Phe	Phe	Gly	Gln	180	185	190	
Phe	Ser	Val	Arg	Gly	Tyr	Val	Asn	Tyr	Asp	Lys	His	Val	Ala	Lys	Tyr	195	200	205	

09765272.012201



Leu Lys Ile Leu Pro Asp Gln Phe Ser Tyr Gln Ala Ile Glu Asp Val  
 210 215 220  
 Val Lys Ala Asp Ala Glu Lys Asn Thr Ser Asn Asn Glu Met Gly Met  
 225 230 235 240  
 Glu Asn Tyr Phe Tyr Asn Glu Gln Ile Lys Lys Asp Leu Lys Lys Leu  
 245 250 255  
 Lys Asp Ser Gln Lys Ser Phe Thr Tyr Leu Lys Ser Pro Glu Tyr Asn  
 260 265 270  
 Xaa Leu Gln Leu Val Leu Thr Gln Phe Ser Lys Ser Lys Val Asn Pro  
 275 280 285  
 Ile Phe Ile Ile Pro Pro Val Asn Lys Lys Trp Met Xaa Tyr Ala Gly  
 290 295 300  
 Leu Arg Glu Asp Met Tyr Gln Gln Thr Val Gln Lys Ile Arg Tyr Gln  
 305 310 315 320  
 Leu Glu Ser Gln Gly Phe Thr Asn Ile Ala Asp Phe Ser Lys Asp Gly  
 325 330 335  
 Gly Glu Pro Phe Phe Met Lys Asp Thr Ile His Leu Gly Trp Leu Gly  
 340 345 350  
 Trp Leu Ala Phe Asp Lys Ala Val Asp Pro Phe Leu Ser Asn Pro Thr  
 355 360 365  
 Pro Ala Pro Thr Tyr His Leu Asn Glu Arg Phe Phe Ser Lys Asp Trp  
 370 375 380  
 Ala Thr Tyr Asp Gly Asp Val Lys Glu  
 385 390

## (2) INFORMATION FOR SEQ ID NO: 59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GGTTTTGAGA AAGTATTTGC AGGGGGCCCT GATTGAGTCG ATTGAGCAAG TGGAAAATGA	60
CCGTATTGTG GAAATTACAG TTTCCAATAA AAACGAGATT GGAGACCATA TCCAGGCTAC	120
CTTGATTATC GAAATTATGG GGAAACACAG TAATATTCTA CTGGTCGATA AAAGCAGTCA	180
TAAAATCCTC GAAGTTATCA AACACGTCGG CTTTTCACAA AATAGCTACC GCACCTTACT	240
TCCAGGATCG ACCTATATCG CTCCGCCAAG TACAAAATCT CTCAATCCTT TTACTIONTCAA	300
GGATGAAAAG CTCTTTGAAA TCCTGCAAAC CCAAGAACTA ACAGCAAAAA ATCTTCAAAG	360
CCTCTTTCAA GGTCTGGGAC GCGATACGGC AAATGAATTG GAAAGGATAC TGGTTAGTGA	420

09765272.012201

AAACTTTCC GCTTCCGAA ATTTTTTCAA TCAAGAAACC AAGCCATGCT TGACTGAGAC 480  
 TTCCTTCAGT CCAGTTCCTT TTGCAAATCA GGTGGGAGAG CCTTTTGCAA ATCTTTCTGA 540  
 TTTGTTGGAC ACCTACTATA AGGATAAGGC TGAGCGCGAC CGCGTCAAAC AGCAGGCCAG 600  
 TGAAGTGAAT CGTCGTGTTG AAAATGAACT TCAGAAAAAC CGACACAAAC TCAAAAAACA 660  
 GGAAAAAGAG TTACTGGCGA CAGACAACGC TGAAGAATTT CGTCAAAAAG GAGAATTGCT 720  
 GACAACCTTC CTCCACCAAG TGCCTAACGA CCAAGACCAG GTTATCCTAG ACAACTACTA 780  
 TACCAACCAA CCTATCATGA TTGCGCTTGA TAAGGCTCTG ACTCCCAACC AGAATGCCCA 840  
 ACGCTATTTT AAACGGTATC AGAAACTCAA AGAAGCTGTC AAATACTTGA CTGATTTGAT 900  
 TGAAGAAACC AAAGCCACTA TTCTCTATCT GGAAAGTGTA GAAACCGTCC TCAACCAAGC 960  
 TGGACTGGAA GAAATCGCTG AAATCCGTGA AGAATTGATT CAAACAGGTT TTATCCGCAG 1020  
 AAGACAACGG GAGAAAATCC AGAAACGCAA AAAACTAGAA CAATATCTAG CAAGCGATGG 1080  
 CAAAACCATC ATCTATGTCG GACGAAACAA TCTTCAAAT GAGGAATTGA CCTTTAAAT 1140  
 GGCCCGCAAG GAGGAACTTT GGTTCATGC TAAGGACATT CCTGGAAGCC ATGTTGTCAT 1200  
 CTCAGGAAAT CTTGACCCAT CTGATGCAGT CAAGACAGAC GCAGCAGAGT TAGCTGCCTA 1260  
 CTTCTCTCAA GGGCGCCTGT CGAATCTGGT GCAGGTAGAT ATGATTGAAG TCAAAAAACT 1320  
 CAATAAACCA ACTGGTGGAA AACCCGGCTT TGTCACCTAC ACAGGACAAA AGACCCTCCG 1380  
 CGTCACACCA GACTCCAAAA AAATTGCATC CATGAAAAAA TCC 1423

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Val Leu Arg Lys Tyr Leu Gln Gly Ala Leu Ile Glu Ser Ile Glu Gln  
 1 5 10 15

Val Glu Asn Asp Arg Ile Val Glu Ile Thr Val Ser Asn Lys Asn Glu  
 20 25 30

Ile Gly Asp His Ile Gln Ala Thr Leu Ile Ile Glu Ile Met Gly Lys  
 35 40 45

His Ser Asn Ile Leu Leu Val Asp Lys Ser Ser His Lys Ile Leu Glu  
 50 55 60

Val Ile Lys His Val Gly Phe Ser Gln Asn Ser Tyr Arg Thr Leu Leu  
 65 70 75 80

Pro Gly Ser Thr Tyr Ile Ala Pro Pro Ser Thr Lys Ser Leu Asn Pro

09765272 012201

85

90

95

Phe Thr Ile Lys Asp Glu Lys Leu Phe Glu Ile Leu Gln Thr Gln Glu  
100— 105 110

Leu Thr Ala Lys Asn Leu Gln Ser Leu Phe Gln Gly Leu Gly Arg Asp  
115 120 125

Thr Ala Asn Glu Leu Glu Arg Ile Leu Val Ser Glu Lys Leu Ser Ala  
130 135 140

Phe Arg Asn Phe Phe Asn Gln Glu Thr Lys Pro Cys Leu Thr Glu Thr  
145 150 155 160

Ser Phe Ser Pro Val Pro Phe Ala Asn Gln Val Gly Glu Pro Phe Ala  
165 170 175

Asn Leu Ser Asp Leu Leu Asp Thr Tyr Tyr Lys Asp Lys Ala Glu Arg  
180 185 190

Asp Arg Val Lys Gln Gln Ala Ser Glu Leu Ile Arg Arg Val Glu Asn  
195 200 205

Glu Leu Gln Lys Asn Arg His Lys Leu Lys Lys Gln Glu Lys Glu Leu  
210 215 220

Leu Ala Thr Asp Asn Ala Glu Glu Phe Arg Gln Lys Gly Glu Leu Leu  
225 230 235 240

Thr Thr Phe Leu His Gln Val Pro Asn Asp Gln Asp Gln Val Ile Leu  
245 250 255

Asp Asn Tyr Tyr Thr Asn Gln Pro Ile Met Ile Ala Leu Asp Lys Ala  
260 265 270

Leu Thr Pro Asn Gln Asn Ala Gln Arg Tyr Phe Lys Arg Tyr Gln Lys  
275 280 285

Leu Lys Glu Ala Val Lys Tyr Leu Thr Asp Leu Ile Glu Glu Thr Lys  
290 295 300

Ala Thr Ile Leu Tyr Leu Glu Ser Val Glu Thr Val Leu Asn Gln Ala  
305 310 315 320

Gly Leu Glu Glu Ile Ala Glu Ile Arg Glu Glu Leu Ile Gln Thr Gly  
325 330 335

Phe Ile Arg Arg Arg Gln Arg Glu Lys Ile Gln Lys Arg Lys Lys Leu  
340 345 350

Glu Gln Tyr Leu Ala Ser Asp Gly Lys Thr Ile Ile Tyr Val Gly Arg  
355 360 365

Asn Asn Leu Gln Asn Glu Glu Leu Thr Phe Lys Met Ala Arg Lys Glu  
370 375 380

Glu Leu Trp Phe His Ala Lys Asp Ile Pro Gly Ser His Val Val Ile  
385 390 395 400

Ser Gly Asn Leu Asp Pro Ser Asp Ala Val Lys Thr Asp Ala Ala Glu  
405 410 415

Leu Ala Ala Tyr Phe Ser Gln Gly Arg Leu Ser Asn Leu Val Gln Val

09765272.012201

420

425

430

Asp Met Ile Glu Val Lys Lys Leu Asn Lys Pro Thr Gly Gly Lys Pro  
 435 440 445

Gly Phe Val Thr Tyr Thr Gly Gln Lys Thr Leu Arg Val Thr Pro Asp  
 450 455 460

Ser Lys Lys Ile Ala Ser Met Lys Lys Ser  
 465 470

## (2) INFORMATION FOR SEQ ID NO: 61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACAACATTT ACTATCCATA CAGTAGAGTC AGCACCAGCA GAAGTGAAAG AAATTCTTGA	60
AACAGTAGAA AAAGACAACA ATGGCTATAT TCCCAACCTA ATCGGTCTCT TGGCCAATGC	120
CCCGACTGTT TTAGAAGCCT ACCAAATTGT CTCATCTATC CACCGTCGCA ACAGCCTGAC	180
ACCCGTTGAG CGTGAAGTGG TGCAAATCAC GGCAGCCGTG ACCAATGGTT GTGCCTTCTG	240
TGTCGCAGGT CACACAGCCT TTTCCATCAA ACAAATCCAG ATGAATGATG ACTTGATTCA	300
AGCTCTTCGC AATCGTACTC CAATTGAAAC AGATCCTAAA TTGGATACCC TAGCTAAGTT	360
TACCTTGGCA GTTATCAATA CCAAGGGTCG TGTAGGAGAT GAAGCCTTGT CTGAGTTTTT	420
AGAAGCTGGC TACTCTCAAC AAAATGCCTT GGATGTGGTT TTTGGTGTCA GCCTAGCAAT	480
CCTCTGTAAC TATGCCAACA ACTTAGCTAA TACACCAATT AATCCAGAAT TGCAACCTTA	540
TGCC	544

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Thr Thr Phe Thr Ile His Thr Val Glu Ser Ala Pro Ala Glu Val Lys  
 1 5 10 15

Glu Ile Leu Glu Thr Val Glu Lys Asp Asn Asn Gly Tyr Ile Pro Asn  
 20 25 30

Leu Ile Gly Leu Leu Ala Asn Ala Pro Thr Val Leu Glu Ala Tyr Gln

05765272.012201

35

40

45

Ile Val Ser Ser Ile His Arg Arg Asn Ser Leu Thr Pro Val Glu Arg  
 50 55 60

Glu Val Val Gln Ile Thr Ala Ala Val Thr Asn Gly Cys Ala Phe Cys  
 65 70 75 80

Val Ala Gly His Thr Ala Phe Ser Ile Lys Gln Ile Gln Met Asn Asp  
 85 90 95

Asp Leu Ile Gln Ala Leu Arg Asn Arg Thr Pro Ile Glu Thr Asp Pro  
 100 105 110

Lys Leu Asp Thr Leu Ala Lys Phe Thr Leu Ala Val Ile Asn Thr Lys  
 115 120 125

Gly Arg Val Gly Asp Glu Ala Leu Ser Glu Phe Leu Glu Ala Gly Tyr  
 130 135 140

Thr Gln Gln Asn Ala Leu Asp Val Val Phe Gly Val Ser Leu Ala Ile  
 145 150 155 160

Leu Cys Asn Tyr Ala Asn Asn Leu Ala Asn Thr Pro Ile Asn Pro Glu  
 165 170 175

Leu Gln Pro Tyr Ala  
 180

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGCTAAGGAA AGAGTGGATG TACTAGCTTA TAAACAGGGG TTGTTTGAAA CGAGAGAGCA	60
GGCCAAGCGA GGTGTGATGG CTGGCCTAGT CGTAGCAGTC CTTAATGGAG AACGGTTTGA	120
CAAGCCAGGA GAGAAAATTC CAGATGACAC CGAATTAAAA CTCAAGGGGG AGAAACTCAA	180
GTATGTCAGC CGTGGTGGTT TGAAACTGGA AAAGGCCTTG CAGGTCTTTG ATTTGTCGGT	240
GGATGGCGCG ACTACGATTG ATATCGGGGC CTCTACTGGA GGTTTTACCG ATGTCATGCT	300
ACAGAATAGT GCCAAGTTGG TCTTTGCAGT CGATGTTGGT ACCAATCAGT TGGCTTGGAA	360
ATTACGCCAA GACCCACGAG TTGTCAGCAT GGAGCAGTTC AATTTCGCT ATGCTGAAAA	420
GACTGATTTC GAGCAGGAGC CGAGCTTTGC CAGTATTGAT GTGAGTTTCA TTTCCCTTAG	480
TCTGATTTTG CCAGCCTTGC ACCGTGTCTT GGCTGATCAA GGTCAGGTGG TAGCACTTGT	540
CAAACCTCAG TTTGAGGCAG GACGTGAGCA GATTGGGAAA AATGGAATTA TTCGAGATGC	600
TAAGGTTTCAT CAGAATGTCC TTGAATCTGT AACAGCTATG GCAGTAGAGG TAGGTTTTTC	660

09765272.012201

AGTCCTTGGC TTGGACTTTT CTCCCATCCA AGGTGGACAT GGAAATATTG AATTTTTCAGC 720  
 GTATTTGAAA AAAGAAAAGT CAGCAAGCAA TCAGATTCTT GCTGAGATTA AAGAAGCAGT 780  
 AGAGAGGGCG CATAGTCAAT TTAAAAATGA A 811

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala Lys Glu Arg Val Asp Val Leu Ala Tyr Lys Gln Gly Leu Phe Glu  
 1 5 10 15  
 Thr Arg Glu Gln Ala Lys Arg Gly Val Met Ala Gly Leu Val Val Ala  
 20 25 30  
 Val Leu Asn Gly Glu Arg Phe Asp Lys Pro Gly Glu Lys Ile Pro Asp  
 35 40 45  
 Asp Thr Glu Leu Lys Leu Lys Gly Glu Lys Leu Lys Tyr Val Ser Arg  
 50 55 60  
 Gly Gly Leu Lys Leu Glu Lys Ala Leu Gln Val Phe Asp Leu Ser Val  
 65 70 75 80  
 Asp Gly Ala Thr Thr Ile Asp Ile Gly Ala Ser Thr Gly Gly Phe Thr  
 85 90 95  
 Asp Val Met Leu Gln Asn Ser Ala Lys Leu Val Phe Ala Val Asp Val  
 100 105 110  
 Gly Thr Asn Gln Leu Ala Trp Lys Leu Arg Gln Asp Pro Arg Val Val  
 115 120 125  
 Ser Met Glu Gln Phe Asn Phe Arg Tyr Ala Glu Lys Thr Asp Phe Glu  
 130 135 140  
 Gln Glu Pro Ser Phe Ala Ser Ile Asp Val Ser Phe Ile Ser Leu Ser  
 145 150 155 160  
 Leu Ile Leu Pro Ala Leu His Arg Val Leu Ala Asp Gln Gly Gln Val  
 165 170 175  
 Val Ala Leu Val Lys Pro Gln Phe Glu Ala Gly Arg Glu Gln Ile Gly  
 180 185 190  
 Lys Asn Gly Ile Ile Arg Asp Ala Lys Val His Gln Asn Val Leu Glu  
 195 200 205  
 Ser Val Thr Ala Met Ala Val Glu Val Gly Phe Ser Val Leu Gly Leu  
 210 215 220  
 Asp Phe Ser Pro Ile Gln Gly Gly His Gly Asn Ile Glu Phe Leu Ala  
 225 230 235 240

09765272.012201

Tyr Leu Lys Lys Glu Lys Ser Ala Ser Asn Gln Ile Leu Ala Glu Ile  
 245 250 255

Lys Glu Ala Val Glu Arg Ala His Ser Gln Phe Lys Asn Glu  
 260 265 270

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTGTTCTAT GAACCTGGTC GTCACCAAGC TGGTCAGGTT AAGAAAGAGT CTAATCGAGT	60
TTCTTATATA GATGGTGATC AGGCTGGTCA AAAGGCAGAA AACTTGACAC CAGATGAAGT	120
CAGTAAGAGG GAGGGGATCA ACGCCGAACA AATNGTNATC AAGATTACGG ATCAAGGTTA	180
TGTGACCTCT CATGGAGACC ATTATCATTA CTATAATGGC AAGGTTCTTT ATGATGCCAT	240
CATCAGTGAA GAGCTCCTCA TGAAAGATCC GAATTATCAG TTGAAGGATT CAGACATTGT	300
CAATGAAATC AAGGGTGGTT ATGTCATTAA GGTAAACGGT AAATACTATG TNTACCTTAA	360
GGATGCAGCT CATGCGGATA ATATTCGGAC AAAAGAAGAG ATTAAACGTC AGAAGCAGGA	420
ACGCAGTCAT AATCATAACT CAAGAGCAGA TAATGCTGTT GCTGCAGCCA GAGCCCAAGG	480
ACGTTATACA ACGGATGATG GGTATATCTT CAATGCATCT GATATCATTG AGGACACGGG	540
TGATGCTTAT ATCGTTCCTC ACGGCGACCA TTACCATTAC ATTCCTAAGA ATGAGTTATC	600
AGCTAGCGAG TTAGCTGCTG CAGAAGCCTA TTGGAATGGG AAGCAGGGAT CTCGTCCTTC	660
TTCAAGTTCT AGTTATAATG CAAATCCAGC TCAACCAAGA TTGTCAGAGA ACCACAATCT	720
GACTGTCACT CCAACTTATC ATCAAAATCA AGGGGAAAAC ATTTCAAGCC TTTTACGTGA	780
ATTGTATGCT AAACCCTTAT CAGAACGCCA TGTGGAATCT GATGGCCTTA TTTTCGACCC	840
AGCGCAAATC ACAAGTCGAA CCGCCAGAGG TGTAGCTGTC CCTCATGGTA ACCATTACCA	900
CTTTATCCCT TATGAACAAA TGTCTGAATT GGAAAAACGA ATTGCTCGTA TTATTCCCCT	960
TCGTTATCGT TCAAACCATT GGGTACCAGA TTCAAGACCA GAACAACCAA GTCCACAATC	1020
GACTCCGGAA CCTAGTCCAA GTCCGCAACC TGCACCAAAT CCTCAACCAG CTCCAAGCAA	1080
TCCAATTGAT GAGAAATTGG TCAAAGAAGC TGTTTCGAAA GTAGGCGATG GTTATGTCTT	1140
TGAGGAGAAT GGAGTTTCTC GTTATATCCC AGCCAAGGAT CTTTCAGCAG AAACAGCAGC	1200
AGGCATTGAT AGCAAACCTGG CCAAGCAGGA AAGTTTATCT CATAAGCTAG GAGCTAAGAA	1260
AACTGACCTC CCATCTAGTG ATCGAGAATT TTACAATAAG GCTTATGACT TACTAGCAAG	1320

09765272.012201

AATTCACCAA GATTTACTTG ATAATAAAGG TCGACAAGTT GATTTTGAGG CTTTGGATAA 1380  
 CCTGTTGGAA CGACTCAAGG ATGTCNCAAG TGATAAAGTC AAGTTAGTGG ANGATATTCT 1440  
 TGCCTTCTTA GCTCCGATTC GTCATCCAGA ACGTTTAGGA AAACCAAATG CGCAAATTAC 1500  
 CTACACTGAT GATGAGATTC AAGTAGCCAA GTTGGCAGGC AAGTACACAA CAGAAGACGG 1560  
 TTATATCTTT GATCCTCGTG ATATAACCAG TGATGAGGGG GATGCCTATG TAACTCCACA 1620  
 TATGACCCAT AGCCACTGGA TTAATAAAGA TAGTTTGTCT GAAGCTGAGA GAGCGGCAGC 1680  
 CCAGGCTTAT GCTAAAGAGA AAGGTTTGAC CCCTCCTTCG ACAGACCATC AGGATTTCAGG 1740  
 AAATACTGAG GCAAAAGGAG CAGAAGCTAT CTACAACCGC GTGAAAGCAG CTAAGAAGGT 1800  
 GCCACTTGAT CGTATGCCTT ACAATCTTCA ATATACTGTA GAAGTCAAAA ACGGTAGTTT 1860  
 AATCATACCT CATTATGACC ATTACCATAA CATCAAATTT GAGTGGTTTG ACGAAGGCCT 1920  
 TTATGAGGCA CCTAAGGGGT ATACTCTTGA GGATCTTTTG GCGACTGTCA AGTACTATGT 1980  
 CGAACATCCA AACGAACGTC CGCATTGAGA TAATGGTTTT GGTAACGCTA GCGACCATGT 2040  
 TCAAAGAAAC AAAAATGGTC AAGCTGATAC CAATCAAACG GAAAAACCAA GCGAGGAGAA 2100  
 ACCTCAGACA GAAAAACCTG AGGAAGAAAC CCCTCGAGAA GAGAAACCGC AAAGCGAGAA 2160  
 ACCAGAGTCT CAAAACCAA CAGAGGAACC AGAAGAATCA CCAGAGGAAT CAGAAGAACC 2220  
 TCAGGTCGAG ACTGAAAAGG TTGAAGAAAA ACTGAGAGAG GCTGAAGATT TACTTGAAAA 2280  
 AATCCAGGAT 2290

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu  
 1 5 10 15  
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala  
 20 25 30  
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala  
 35 40 45  
 Glu Gln Xaa Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His  
 50 55 60  
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile  
 65 70 75 80  
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp

09765272.012201



85

90

95

Ser	Asp	Ile	Val	Asn	Glu	Ile	Lys	Gly	Gly	Tyr	Val	Ile	Lys	Val	Asn		
			100					105					110				
Gly	Lys	Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala	Asp	Asn	Ile		
		115					120					125					
Arg	Thr	Lys	Glu	Glu	Ile	Lys	Arg	Gln	Lys	Gln	Glu	Arg	Ser	His	Asn		
	130					135					140						
His	Asn	Ser	Arg	Ala	Asp	Asn	Ala	Val	Ala	Ala	Ala	Arg	Ala	Gln	Gly		
145					150					155					160		
Arg	Tyr	Thr	Thr	Asp	Asp	Gly	Tyr	Ile	Phe	Asn	Ala	Ser	Asp	Ile	Ile		
				165					170					175			
Glu	Asp	Thr	Gly	Asp	Ala	Tyr	Ile	Val	Pro	His	Gly	Asp	His	Tyr	His		
			180					185					190				
Tyr	Ile	Pro	Lys	Asn	Glu	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala	Glu		
		195					200					205					
Ala	Tyr	Trp	Asn	Gly	Lys	Gln	Gly	Ser	Arg	Pro	Ser	Ser	Ser	Ser	Ser		
	210					215					220						
Tyr	Asn	Ala	Asn	Pro	Ala	Gln	Pro	Arg	Leu	Ser	Glu	Asn	His	Asn	Leu		
225					230					235					240		
Thr	Val	Thr	Pro	Thr	Tyr	His	Gln	Asn	Gln	Gly	Glu	Asn	Ile	Ser	Ser		
				245					250					255			
Leu	Leu	Arg	Glu	Leu	Tyr	Ala	Lys	Pro	Leu	Ser	Glu	Arg	His	Val	Glu		
			260					265					270				
Ser	Asp	Gly	Leu	Ile	Phe	Asp	Pro	Ala	Gln	Ile	Thr	Ser	Arg	Thr	Ala		
		275					280					285					
Arg	Gly	Val	Ala	Val	Pro	His	Gly	Asn	His	Tyr	His	Phe	Ile	Pro	Tyr		
	290					295					300						
Glu	Gln	Met	Ser	Glu	Leu	Glu	Lys	Arg	Ile	Ala	Arg	Ile	Ile	Pro	Leu		
305					310					315					320		
Arg	Tyr	Arg	Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Pro	Glu	Gln	Pro		
				325					330					335			
Ser	Pro	Gln	Ser	Thr	Pro	Glu	Pro	Ser	Pro	Ser	Pro	Gln	Pro	Ala	Pro		
			340					345					350				
Asn	Pro	Gln	Pro	Ala	Pro	Ser	Asn	Pro	Ile	Asp	Glu	Lys	Leu	Val	Lys		
		355					360					365					
Glu	Ala	Val	Arg	Lys	Val	Gly	Asp	Gly	Tyr	Val	Phe	Glu	Glu	Asn	Gly		
	370					375					380						
Val	Ser	Arg	Tyr	Ile	Pro	Ala	Lys	Asp	Leu	Ser	Ala	Glu	Thr	Ala	Ala		
385					390				395						400		
Gly	Ile	Asp	Ser	Lys	Leu	Ala	Lys	Gln	Glu	Ser	Leu	Ser	His	Lys	Leu		
				405					410					415			
Gly	Ala	Lys	Lys	Thr	Asp	Leu	Pro	Ser	Ser	Asp	Arg	Glu	Phe	Tyr	Asn		

097655272.012201

420

425

430

Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn  
 435 440 445  
 Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg  
 450 455 460  
 Leu Lys Asp Val Xaa Ser Asp Lys Val Lys Leu Val Xaa Asp Ile Leu  
 465 470 475 480  
 Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn  
 485 490 495  
 Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala  
 500 505 510  
 Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile  
 515 520 525  
 Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser  
 530 535 540  
 His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala  
 545 550 555 560  
 Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His  
 565 570 575  
 Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn  
 580 585 590  
 Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn  
 595 600 605  
 Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His  
 610 615 620  
 Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu  
 625 630 635 640  
 Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val  
 645 650 655  
 Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly  
 660 665 670  
 Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala  
 675 680 685  
 Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu  
 690 695 700  
 Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys  
 705 710 715 720  
 Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Ser Pro Glu Glu  
 725 730 735  
 Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg  
 740 745 750  
 Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp

09765272 012201

755

760

## (2) INFORMATION FOR SEQ ID NO: 67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TTATAAGGGT GAATTAGAAA AAGGATACCA ATTTGATGGT TGGGAAATTT CTGGTTTCGA 60  
 AGGTAAAAAA GACGCTGGCT ATGTTATTAA TCTATCAAAA GATACCTTTA TAAACCTGT 120  
 ATTCAAGAAA ATAGAGGAGA AAAAGGAGGA AGAAAATAAA CCTACTTTTG ATGTATCGAA 180  
 AAAGAAAGAT AACCCACAAG TAAACCATAG TCAATTAAAT GAAAGTCACA GAAAAGAGGA 240  
 TTTACAAAGA GAAGAGCATT CACAAAAATC TGATTCAACT AAGGATGTTA CAGCTACAGT 300  
 TCTTGATAAA AACAAATATCA GTAGTAAATC AACTACTAAC AATCCTAATA AG 352

## (2) INFORMATION FOR SEQ ID NO: 68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Tyr Lys Gly Glu Leu Glu Lys Gly Tyr Gln Phe Asp Gly Trp Glu Ile  
 1 5 10 15  
 Ser Gly Phe Glu Gly Lys Lys Asp Ala Gly Tyr Val Ile Asn Leu Ser  
 20 25 30  
 Lys Asp Thr Phe Ile Lys Pro Val Phe Lys Lys Ile Glu Glu Lys Lys  
 35 40 45  
 Glu Glu Glu Asn Lys Pro Thr Phe Asp Val Ser Lys Lys Lys Asp Asn  
 50 55 60  
 Pro Gln Val Asn His Ser Gln Leu Asn Glu Ser His Arg Lys Glu Asp  
 65 70 75 80  
 Leu Gln Arg Glu Glu His Ser Gln Lys Ser Asp Ser Thr Lys Asp Val  
 85 90 95  
 Thr Ala Thr Val Leu Asp Lys Asn Asn Ile Ser Ser Lys Ser Thr Thr  
 100 105 110  
 Asn Asn Pro Asn Lys  
 115

09765272.012201

## (2) INFORMATION FOR SEQ ID NO: 69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GAATGTTTCAG GCTCAAGAAA GTTCAGGAAA TAAATCCAC TTTATCAATG TTCAAGAAGG 60

TGGCAGTGAT GCGATTATTC TTGAAAGCAA TGGACATTTT GCCATGGTGG ATACAGGAGA 120

AGATTATGAT TTCCCAGATG GAAGTGATTC TCGCTATCCA TGGAGAGAAG GAATTGAAAC 180

GTCTTATAAG CATGTTCTAA CAGACCGTGT CTTTCGTCGT TTGAAGGAAT TGGGTGTCCA 240

AAACTTGAT TTTATTTTGG TGACCCATAC CCACAGTGAT CATATTGGAA ATGTTGATGA 300

ATTACTGTCT ACCTATCCAG TTGACCGAGT CTATCTTAAG AAATATAGTG ATAGTCGTAT 360

TACTAATTCT GAACGTCTAT GGGATAATCT GTATGGCTAT GATAAGGTTT TACAGACTGC 420

TGCAGAAAAA GGTGTTTCAG TTATTCAAAA TATCACACAA GGGGATGCTC ATTTTCAGTT 480

TGGGGACATG GATATTCAGC TCTATAATTA TGAAAATGAA ACTGATTCAT CGGGTGAATT 540

AAAGAAAATT TGGGATGACA ATTCCAATTC CTTGATTAGC GTGGTGAAAG TCAATGGCAA 600

GAAAATTTAC CTTGGGGGCG ATTTAGATAA TGTTTCATGGA GCAGAAGACA AGTATGGTCC 660

TCTCATTGGA AAAGTTGATT TGATGAAGTT TAATCATCAC CATGATACCA ACAAATCAAA 720

TACCAAGGAT TTCATTAAAA ATTTGAGTCC GAGTTTGATT GTTCAAACCT CGGATAGTCT 780

ACCTTGGAAT AATGGTGTG ATAGTGAGTA TGTTAATTGG CTCAAAGAAC GAGGAATTGA 840

GAGAATCAAC GCAGCCAGCA AAGACTATGA TGCAACAGTT TTTGATATTC GAAAAGACGG 900

TTTTGTCAAT ATTTCAACAT CCTACAAGCC GATTCCAAGT TTTCAAGCTG GTTGGCATAA 960

GAGTGCATAT GGGAACGGT GGTATCAAGC GCCTGATTCT ACAGGAGAGT ATGCTGTCTGG 1020

TTGGAATGAA ATCGAAGGTG AATGGTATTA CTTTAACCAA ACGGGTATCT TGTTACAGAA 1080

TCAATGGAAT AAATGGAACA ATCATTGGTT CTATTTGACA GACTCTGGTG CTTCTGCTAA 1140

AAATTGGAAG AAAATCGCTG GAATCTGGTA TTATTTTAAC AAAGAAAACC AGATGGAAAT 1200

TGGTTGGATT CAAGATAAAG AGCAGTGGTA TTATTTGGAT GTTGATGGTT CTATGAAGAC 1260

AGGATGGCTT CAATATATGG GGCAATGGTA TTA CTTTGCT CCATCAGGGG AA 1312

## (2) INFORMATION FOR SEQ ID NO: 70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

09765272.012201

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ-ID NO:70:

Asn	Val	Gln	Ala	Gln	Glu	Ser	Ser	Gly	Asn	Lys	Ile	His	Phe	Ile	Asn	
1				5					10					15		
Val	Gln	Glu	Gly	Gly	Ser	Asp	Ala	Ile	Ile	Leu	Glu	Ser	Asn	Gly	His	
			20					25					30			
Phe	Ala	Met	Val	Asp	Thr	Gly	Glu	Asp	Tyr	Asp	Phe	Pro	Asp	Gly	Ser	
		35					40					45				
Asp	Ser	Arg	Tyr	Pro	Trp	Arg	Glu	Gly	Ile	Glu	Thr	Ser	Tyr	Lys	His	
	50					55					60					
Val	Leu	Thr	Asp	Arg	Val	Phe	Arg	Arg	Leu	Lys	Glu	Leu	Gly	Val	Gln	
65					70					75					80	
Lys	Leu	Asp	Phe	Ile	Leu	Val	Thr	His	Thr	His	Ser	Asp	His	Ile	Gly	
				85					90					95		
Asn	Val	Asp	Glu	Leu	Leu	Ser	Thr	Tyr	Pro	Val	Asp	Arg	Val	Tyr	Leu	
			100					105					110			
Lys	Lys	Tyr	Ser	Asp	Ser	Arg	Ile	Thr	Asn	Ser	Glu	Arg	Leu	Trp	Asp	
		115					120					125				
Asn	Leu	Tyr	Gly	Tyr	Asp	Lys	Val	Leu	Gln	Thr	Ala	Ala	Glu	Lys	Gly	
	130					135					140					
Val	Ser	Val	Ile	Gln	Asn	Ile	Thr	Gln	Gly	Asp	Ala	His	Phe	Gln	Phe	
145					150					155					160	
Gly	Asp	Met	Asp	Ile	Gln	Leu	Tyr	Asn	Tyr	Glu	Asn	Glu	Thr	Asp	Ser	
				165					170					175		
Ser	Gly	Glu	Leu	Lys	Lys	Ile	Trp	Asp	Asp	Asn	Ser	Asn	Ser	Leu	Ile	
			180					185					190			
Ser	Val	Val	Lys	Val	Asn	Gly	Lys	Lys	Ile	Tyr	Leu	Gly	Gly	Asp	Leu	
		195					200					205				
Asp	Asn	Val	His	Gly	Ala	Glu	Asp	Lys	Tyr	Gly	Pro	Leu	Ile	Gly	Lys	
	210					215					220					
Val	Asp	Leu	Met	Lys	Phe	Asn	His	His	His	Asp	Thr	Asn	Lys	Ser	Asn	
225					230					235					240	
Thr	Lys	Asp	Phe	Ile	Lys	Asn	Leu	Ser	Pro	Ser	Leu	Ile	Val	Gln	Thr	
				245					250					255		
Ser	Asp	Ser	Leu	Pro	Trp	Lys	Asn	Gly	Val	Asp	Ser	Glu	Tyr	Val	Asn	
			260					265					270			
Trp	Leu	Lys	Glu	Arg	Gly	Ile	Glu	Arg	Ile	Asn	Ala	Ala	Ser	Lys	Asp	
		275					280				285					
Tyr	Asp	Ala	Thr	Val	Phe	Asp	Ile	Arg	Lys	Asp	Gly	Phe	Val	Asn	Ile	
	290					295					300					

09765272.012201

Ser Thr Ser Tyr Lys Pro Ile Pro Ser Phe Gln Ala Gly Trp His Lys  
305 310 315 320

Ser Ala Tyr Gly Asn Trp Trp Tyr Gln Ala Pro Asp Ser Thr Gly Glu  
325 330 335

Tyr Ala Val Gly Trp Asn Glu Ile Glu Gly Glu Trp Tyr Tyr Phe Asn  
340 345 350

Gln Thr Gly Ile Leu Leu Gln Asn Gln Trp Lys Lys Trp Asn Asn His  
355 360 365

Trp Phe Tyr Leu Thr Asp Ser Gly Ala Ser Ala Lys Asn Trp Lys Lys  
370 375 380

Ile Ala Gly Ile Trp Tyr Tyr Phe Asn Lys Glu Asn Gln Met Glu Ile  
385 390 395 400

Gly Trp Ile Gln Asp Lys Glu Gln Trp Tyr Tyr Leu Asp Val Asp Gly  
405 410 415

Ser Met Lys Thr Gly Trp Leu Gln Tyr Met Gly Gln Trp Tyr Tyr Phe  
420 425 430

Ala Pro Ser Gly Glu  
435

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTTGGGTGTA ACCCATATCC AGCTCCTTCC AGTCTTGTCT TACTACTTTG TCAATGAATT	60
GAAAAACCAT GAACGCTTGT CTGACTACGC TTCAAGCAAC AGCAACTACA ACTGGGGATA	120
TGACCCTCAA AACTACTTCT CCTTGACTGG TATGTACTCA AGCGATCCTA AGAATCCAGA	180
AAAACGAATC GCAGAATTTA AAAACCTCAT CAACGAAATC CACAAACGTG GTATGGGAGC	240
TATCCTAGAT GTCGTTTATA ACCACACAGC CAAAGTCGAT CTCTTTGAAG ATTTGGAACC	300
AAACTACTAC CACTTTATGG ATGCCGATGG CACACCTCGA ACTAGCTTTG GTGGTGGACG	360
CTTGGGGACA ACCCACCATA TGACCAAACG GCTCCTAATT GACTCTATCA AATACCTAGT	420
TGATACCTAC AAAGTGGATG GCTTCCGTTT CGATATGATG GGAGACCATG ACGCCGCTTC	480
TATCGAAGAA GCTTACAAGG CTGCACGCGC CCTCAATCCA AACCTCATCA TGCTTGGTGA	540
AGGTTGGAGA ACCTATGCCG GTGATGAAAA CATGCCTACT AAAGCTGCTG ACCAAGATTG	600
GATGAAACAT ACCGATACTG TCGCTGTCTT TTCAGATGAC ATCCGTAACA ACCTCAAATC	660
TGGTTATCCA AACGAAGGTC AACCTGCCTT TATCACAGGT GGCAAGCGTG ATGTCAACAC	720

09765272.012201

CATCTTTAAA AATCTCATTG CTCAACCAAC TAACTTTGAA GCTGACAGCC CTGGAGATGT 780  
 CATCCAATAC ATCGCAGCCC ATGATAACTT GACCCTCTTT GACATCATTG CCCAGTCTAT 840  
 CAAAAAAGAC CCAAGCAAGG CTGAGAACTA TGCTGAAATC CACCGTCGTT TACGACTTGG 900  
 AAATCTCATG GTCTTGACAG CTCAAGGAAC TCCATTTATC CACTCCGGTC AGGAATATGG 960  
 ACGTACTAAA CAATTCCTGT ACCCAGCCTA CAAGACTCCA GTAGCAGAGG ATAAGGTTCC 1020  
 AAACAAATCT CACTTGTTGC GTGATAAGGA CGGCAACCCA TTTGACTATC CTTACTTCAT 1080  
 CCATGACTCT TACGATTCTA GTGATGCAGT CAACAAGTTT GACTGGACTA AGGCTACAGA 1140  
 TGGTAAAGCT TATCCTGAAA ATGTCAAGAG CCGTGACTAT ATGAAAGGTT TGATTGCCCT 1200  
 TCGTCAATCT ACAGATGCCT TCCGACTTAA GAGTCTTCAA GATATCAAAG ACCGTGTCCA 1260  
 CCTCATCACT GTCCCAGGCC AAAATGGTGT GGAAAAAGAG GATGTAGTGA TTGGCTACCA 1320  
 AATCACTGCT CCAAACGGCG ATATCTACGC AGTCTTTGTC AATGCGGATG AAAAAGCTCG 1380  
 CGAATTTAAT TTGGGAACTG CCTTTGCACA TCTAAGAAAT GCGGAAGTTT TGGCAGATGA 1440  
 AAACCAAGCA GGACCAGTCG GAATTGCCAA CCCGAAAGGA CTTGAATGGA CTGAAAAAGG 1500  
 CTTGAAATTG AATGCCCTTA CAGCTACTGT TCTTCGAGTC TCTCAAATG GAACTAGCCA 1560  
 TGAGTCAACT GCAGAAGAGA AACCAGACTC AACCCTTCC AAGCCTGAAC ATCAAAATGA 1620  
 AGCTTCTCAC CCTGCACATC AAGACCCAGC TCCAGAAGCT AGACCTGATT CTACTAAACC 1680  
 AGATGCCAAA GTAGCTGATG CGGAAAATAA ACCTAGCCAA GCTACAGCTG ATTCACAAGC 1740  
 TGAACAACCA GCACAAGAAG CACAAGCATC ATCTGTAAAA GAAGCGGTTC GAAACGAATC 1800  
 GGTAGAAAAC TCTAGCAAGG AAAATATACC TGCAACCCCA GATAACAAG CTGAA 1855

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Gly Val Thr His Ile Gln Leu Leu Pro Val Leu Ser Tyr Tyr Phe  
 1 5 10 15  
 Val Asn Glu Leu Lys Asn His Glu Arg Leu Ser Asp Tyr Ala Ser Ser  
 20 25 30  
 Asn Ser Asn Tyr Asn Trp Gly Tyr Asp Pro Gln Asn Tyr Phe Ser Leu  
 35 40 45  
 Thr Gly Met Tyr Ser Ser Asp Pro Lys Asn Pro Glu Lys Arg Ile Ala  
 50 55 60

09765272.012204

Glu Phe Lys Asn Leu Ile Asn Glu Ile His Lys Arg Gly Met Gly Ala  
 65 70 75 80  
 Ile Leu Asp Val Val Tyr Asn His Thr Ala Lys Val Asp Leu Phe Glu  
 85 90 95  
 Asp Leu Glu Pro Asn Tyr Tyr His Phe Met Asp Ala Asp Gly Thr Pro  
 100 105 110  
 Arg Thr Ser Phe Gly Gly Gly Arg Leu Gly Thr Thr His His Met Thr  
 115 120 125  
 Lys Arg Leu Leu Ile Asp Ser Ile Lys Tyr Leu Val Asp Thr Tyr Lys  
 130 135 140  
 Val Asp Gly Phe Arg Phe Asp Met Met Gly Asp His Asp Ala Ala Ser  
 145 150 155 160  
 Ile Glu Glu Ala Tyr Lys Ala Ala Arg Ala Leu Asn Pro Asn Leu Ile  
 165 170 175  
 Met Leu Gly Glu Gly Trp Arg Thr Tyr Ala Gly Asp Glu Asn Met Pro  
 180 185 190  
 Thr Lys Ala Ala Asp Gln Asp Trp Met Lys His Thr Asp Thr Val Ala  
 195 200 205  
 Val Phe Ser Asp Asp Ile Arg Asn Asn Leu Lys Ser Gly Tyr Pro Asn  
 210 215 220  
 Glu Gly Gln Pro Ala Phe Ile Thr Gly Gly Lys Arg Asp Val Asn Thr  
 225 230 235 240  
 Ile Phe Lys Asn Leu Ile Ala Gln Pro Thr Asn Phe Glu Ala Asp Ser  
 245 250 255  
 Pro Gly Asp Val Ile Gln Tyr Ile Ala Ala His Asp Asn Leu Thr Leu  
 260 265 270  
 Phe Asp Ile Ile Ala Gln Ser Ile Lys Lys Asp Pro Ser Lys Ala Glu  
 275 280 285  
 Asn Tyr Ala Glu Ile His Arg Arg Leu Arg Leu Gly Asn Leu Met Val  
 290 295 300  
 Leu Thr Ala Gln Gly Thr Pro Phe Ile His Ser Gly Gln Glu Tyr Gly  
 305 310 315 320  
 Arg Thr Lys Gln Phe Arg Asp Pro Ala Tyr Lys Thr Pro Val Ala Glu  
 325 330 335  
 Asp Lys Val Pro Asn Lys Ser His Leu Leu Arg Asp Lys Asp Gly Asn  
 340 345 350  
 Pro Phe Asp Tyr Pro Tyr Phe Ile His Asp Ser Tyr Asp Ser Ser Asp  
 355 360 365  
 Ala Val Asn Lys Phe Asp Trp Thr Lys Ala Thr Asp Gly Lys Ala Tyr  
 370 375 380  
 Pro Glu Asn Val Lys Ser Arg Asp Tyr Met Lys Gly Leu Ile Ala Leu  
 385 390 395 400

09765272.012201



Arg Gln Ser Thr Asp Ala Phe Arg Leu Lys Ser Leu Gln Asp Ile Lys  
 405 410 415  
 Asp Arg Val His Leu Ile Thr Val Pro Gly Gln Asn Gly Val Glu Lys  
 420 425 430  
 Glu Asp Val Val Ile Gly Tyr Gln Ile Thr Ala Pro Asn Gly Asp Ile  
 435 440 445  
 Tyr Ala Val Phe Val Asn Ala Asp Glu Lys Ala Arg Glu Phe Asn Leu  
 450 455 460  
 Gly Thr Ala Phe Ala His Leu Arg Asn Ala Glu Val Leu Ala Asp Glu  
 465 470 475 480  
 Asn Gln Ala Gly Pro Val Gly Ile Ala Asn Pro Lys Gly Leu Glu Trp  
 485 490 495  
 Thr Glu Lys Gly Leu Lys Leu Asn Ala Leu Thr Ala Thr Val Leu Arg  
 500 505 510  
 Val Ser Gln Asn Gly Thr Ser His Glu Ser Thr Ala Glu Glu Lys Pro  
 515 520 525  
 Asp Ser Thr Pro Ser Lys Pro Glu His Gln Asn Glu Ala Ser His Pro  
 530 535 540  
 Ala His Gln Asp Pro Ala Pro Glu Ala Arg Pro Asp Ser Thr Lys Pro  
 545 550 555 560  
 Asp Ala Lys Val Ala Asp Ala Glu Asn Lys Pro Ser Gln Ala Thr Ala  
 565 570 575  
 Asp Ser Gln Ala Glu Gln Pro Ala Gln Glu Ala Gln Ala Ser Ser Val  
 580 585 590  
 Lys Glu Ala Val Arg Asn Glu Ser Val Glu Asn Ser Ser Lys Glu Asn  
 595 600 605  
 Ile Pro Ala Thr Pro Asp Lys Gln Ala Glu  
 610 615

## (2) INFORMATION FOR SEQ ID NO: 73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TAGTGATGGT ACTTGGAAG GAAAACAGTA TCTGAAAGAA GATGGCAGTC AAGCAGCAAA	60
TGAGTGGGTT TTNGATACTC ATTATCAATC TTGGTTCTAT ATAAAAGCAG ATGCTAACTA	120
TGCTGAAAAT GAATGGCTAA AGCAAGGTGA CGACTATTTT TACCTCAAAT CTGGTGGCTA	180
TATGGCCAAA TCAGAAATGGG TAGAAGACAA GGGAGCCTTT TATTATCTTG ACCAAGATGG	240
AAAGATGAAA AGAAATGCTT GGGTAGGAAC TTCCTATGTT GGTGCAACAG GTGCCAAAGT	300

09765272.012201

AATAGAAGAC TGGGTCTATG ATTCTCAATA CGATGCTTGG TTTTATATCA AAGCAGATGG 360  
 ACAGCACGCA GAGAAAGAAT GGCTCCAAAT TAAAGGGAAG GACTATTATT TCAAATCCGG 420  
 TGGTTATCTA CTGACAAGTC AGTGGATTAA TCAAGCTTAT GTGAATGCTA GTGGTGCCAA 480  
 AGTACAGCAA GGTGCGCTTT TTGACAAACA ATACCAATCT TGGTTTTACA TCAAAGAAAA 540  
 TGGAAACTAT GCTGATAAAG AATGGATTTT CGAGAATGGT CACTATTATT ATCTAAAATC 600  
 CGGTGGCTAC ATGGCAGCCA ATGAATGGAT TTGGGATAAG GAATCTTGGT TTTATCTCAA 660  
 ATTTGATGGG AAAATGGCTG AAAAAGAATG GGTCTACGAT TCTCATAGTC AAGCTTG GTA 720  
 CTA CTCTCAA TCCGGTGGTT ACATGACAGC CAATGAATGG ATTTGGGATA AGGAATCTTG 780  
 GTTTTACCTC AAATCTGATG GGAAATAGC TGAAAAAGAA TGGGTCTACG ATTCTCATAG 840  
 TCAAGCTTGG TACTACTTCA AATCTGGTGG CTACATGGCG AAAAATGAGA CAGTAGATGG 900  
 TTATCAGCTT GGAAGCGATG GTAAATGGCT TGGAGGAAAA ACTACAAATG AAAATGCTGC 960  
 TTACTATCAA GTAGTGCCTG TTACAGCCAA TGTTTATGAT TCAGATGGTG AAAAGCTTTC 1020  
 CTATATATCG CAAGGTAGTG TCGTATGGCT AGATAAGGAT AGAAAAAGTG ATGACAAGCG 1080  
 CTTGGCTATT ACTATTTCTG GTTTGTCAGG CTATATGAAA ACAGAAGATT TACAAGCGCT 1140  
 AGATGCTAGT AAGGACTTTA TCCCTTATTA TGAGAGTGAT GGCCACCGTT TTTATCACTA 1200  
 TGTGGCTCAG AATGCTAGTA TCCCAGTAGC TTCTCATCTT TCTGATATGG AAGTAGGCAA 1260  
 GAAATATTAT TCGGCAGATG GCCTGCATTT TGATGGTTTT AAGCTTGAGA ATCCCTTCCT 1320  
 TTTCAAAGAT TTAACAGAGG CTACAACTA CAGTGCTGAA GAATTGGATA AGGTATTTAG 1380  
 TTTGCTAAAC ATTAACAATA GCCTTTTGGA GAACAAGGGC GCTACTTTTA AGGAAGCCGA 1440  
 AGAACATTAC CATATCAATG CTCTTTATCT CCTTGCCCAT AGTGCCCTAG AAAGTAACTG 1500  
 GGAAGAAGT AAAATTGCCA AAGATAAGAA TAATTTCTTT GGCATTACAG CCTATGATAC 1560  
 GACCCCTTAC CTTTCTGCTA AGACATTTGA TGATGTGGAT AAGGGAATTT TAGGTGCAAC 1620  
 CAAGTGGATT AAGGAAAATT ATATCGATAG GGAAGAAGT TTCCTTGGA ACAAGGCTTC 1680  
 TGGTATGAAT GTGGAATATG CTTAGACCC TTATTGGGGC GAAAAAATTG CTAGTGTGAT 1740  
 GATGAAAATC AATGAGAAGC TAGGTGGCAA AGAT 1774

## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 591 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

09765272.012201

Ser Asp Gly Thr Trp Gln Gly Lys Gln Tyr Leu Lys Glu Asp Gly Ser  
 1 5 10 15  
 Gln Ala Ala Asn Glu Trp Val Xaa Asp Thr His Tyr Gln Ser Trp Phe  
 20 25 30  
 Tyr Ile Lys Ala Asp Ala Asn Tyr Ala Glu Asn Glu Trp Leu Lys Gln  
 35 40 45  
 Gly Asp Asp Tyr Phe Tyr Leu Lys Ser Gly Gly Tyr Met Ala Lys Ser  
 50 55 60  
 Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp Gln Asp Gly  
 65 70 75 80  
 Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val Gly Ala Thr  
 85 90 95  
 Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln Tyr Asp Ala  
 100 105 110  
 Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys Glu Trp Leu  
 115 120 125  
 Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly Tyr Leu Leu  
 130 135 140  
 Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser Gly Ala Lys  
 145 150 155 160  
 Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser Trp Phe Tyr  
 165 170 175  
 Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile Phe Glu Asn  
 180 185 190  
 Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala Ala Asn Glu  
 195 200 205  
 Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe Asp Gly Lys  
 210 215 220  
 Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr  
 225 230 235 240  
 Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp  
 245 250 255  
 Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys  
 260 265 270  
 Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser  
 275 280 285  
 Gly Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly  
 290 295 300  
 Ser Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala  
 305 310 315 320  
 Tyr Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly  
 325 330 335

09765272.012201

Glu Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys  
340 345 350

Asp Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu  
355 360 365

Ser Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys  
370 375 380

Asp Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr  
385 390 395 400

Val Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met  
405 410 415

Glu Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly  
420 425 430

Phe Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr  
435 440 445

Asn Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile  
450 455 460

Asn Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu  
465 470 475 480

Glu His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu  
485 490 495

Glu Ser Asn Trp Gly Arg Ser Lys Ile Ala Lys Asp Lys Asn Asn Phe  
500 505 510

Phe Gly Ile Thr Ala Tyr Asp Thr Thr Pro Tyr Leu Ser Ala Lys Thr  
515 520 525

Phe Asp Asp Val Asp Lys Gly Ile Leu Gly Ala Thr Lys Trp Ile Lys  
530 535 540

Glu Asn Tyr Ile Asp Arg Gly Arg Thr Phe Leu Gly Asn Lys Ala Ser  
545 550 555 560

Gly Met Asn Val Glu Tyr Ala Ser Asp Pro Tyr Trp Gly Glu Lys Ile  
565 570 575

Ala Ser Val Met Met Lys Ile Asn Glu Lys Leu Gly Gly Lys Asp  
580 585 590

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:\_\_\_\_\_

TGGGATTCAA TATGTCAGAG ATGATACTAG AGATAAAGAA GAGGGAATAG AGTATGATGA

CGCTGACAAT GGGGATATTA TTGTAAAAGT AGCGACTAAA CCTAAGGTAG TAACCAAGAA 120  
AATTTCAAGT ACGCGAATTC GTTATGAAAA AGATGAAACA AAAGACCGTA GTGAAAATCC 180  
TGTTACAATT GATGGAGAGG ATGGCTATGT AACTACGACA AGGACCTACG ATGTTAATCC 240  
AGAGACTGGT TATGTTACCG AACAGGTTAC TGTTGATAGA AAAGAAGCCA CGGATACAGT 300  
TATCAAAGTT CCAGCTAAAA GCAAGGTTGA AGAAGTTCTT GTTCCATTTG CTACTAAATA 360  
TGAAGCAGAC AATGACCTTT CTGCAGGACA GGAGCAAGAG ATTACTCTAG GAAAGAATGG 420  
GAAAACAGTT ACAACGATAA CTTATAATGT AGATGGAAAG AGTGGACAAG TAACTGAGAG 480  
TACTTTAAGT CAAAAAAG ACTCtCAAAC AAGAGTTGTT AAAAAAGaA CCArkCCCCA 540  
AGTTCCTGTC CAAGAAATTC CAATCGAAAC AGAATATCTC GATGGCCCaA CTCTTGATAA 600  
AaGTCAAGAA GTAGAAGAAG TAGGAGAAAT TGGTAAATTA CTCTTACTAC AATCTATACT 660  
GGTAGATGAA CGTGATGGAA CAATTGAAGA-AACTACTTCT CGTCAAATTA CTAAAGAGAT 720  
GGTAAAAAGA CGTATAAGGA GAGGGACGAG AGAACCTGAA AAAGTTGTTG TTCCTGAGCA 780  
ATCATCTATT CCTTCGTATC CTGTATCTGT TACATCTAAC CAAGGAACAG ATGTAGCAGT 840  
AGAACCAGCT AAAGCAGTTG CTCCAACAAC AGACTGGAAA CAAGAAAATG GTATGTGGTA 900  
TTTTTATAAT ACTGATGGTT CCATGGCAAC AGGTTGGGTA CAAGTTAATA GTTCATGGTA 960  
CTACCTCAAC AGCAACGGTT CTATGAAAGT CAATCAATGG TTCCAAGTTG GTGGTAAATG 1020  
GTATTATGTA AATACATCGG GTGAGTTAGC GGTCAATACA AGTATAGATG GCTATAGAGT 1080  
CAATGATAAT GGTGAATGGG TCGCT 1105

## (2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 368 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Gly Ile Gln Tyr Val Arg Asp Asp Thr Arg Asp Lys Glu Glu Gly Ile  
1 5 10 15  
Glu Tyr Asp Asp Ala Asp Asn Gly Asp Ile Ile Val Lys Val Ala Thr  
20 25 30  
Lys Pro Lys Val Val Thr Lys Lys Ile Ser Ser Thr Arg Ile Arg Tyr  
35 40 45  
Glu Lys Asp Glu Thr Lys Asp Arg Ser Glu Asn Pro Val Thr Ile Asp  
50 55 60  
Gly Glu Asp Gly Tyr Val Thr Thr Thr Arg Thr Tyr Asp Val Asn Pro  
65 70 75 80

09765272.012201

Glu Thr Gly Tyr Val Thr Glu Gln Val Thr Val Asp Arg Lys Glu Ala  
 85 90 95  
 Thr Asp Thr Val Ile Lys Val Pro Ala Lys Ser Lys Val Glu Glu Val  
 100 105 110  
 Leu Val Pro Phe Ala Thr Lys Tyr Glu Ala Asp Asn Asp Leu Ser Ala  
 115 120 125  
 Gly Gln Glu Gln Glu Ile Thr Leu Gly Lys Asn Gly Lys Thr Val Thr  
 130 135 140  
 Thr Ile Thr Tyr Asn Val Asp Gly Lys Ser Gly Gln Val Thr Glu Ser  
 145 150 155 160  
 Thr Leu Ser Gln Lys Lys Asp Ser Gln Thr Arg Val Val Lys Lys Arg  
 165 170 175  
 Thr Xaa Pro Gln Val Leu Val Gln Glu Ile Pro Ile Glu Thr Glu Tyr  
 180 185 190  
 Leu Asp Gly Pro Thr Leu Asp Lys Ser Gln Glu Val Glu Glu Val Gly  
 195 200 205  
 Glu Ile Gly Lys Leu Leu Leu Leu Gln Ser Ile Leu Val Asp Glu Arg  
 210 215 220  
 Asp Gly Thr Ile Glu Glu Thr Thr Ser Arg Gln Ile Thr Lys Glu Met  
 225 230 235 240  
 Val Lys Arg Arg Ile Arg Arg Gly Thr Arg Glu Pro Glu Lys Val Val  
 245 250 255  
 Val Pro Glu Gln Ser Ser Ile Pro Ser Tyr Pro Val Ser Val Thr Ser  
 260 265 270  
 Asn Gln Gly Thr Asp Val Ala Val Glu Pro Ala Lys Ala Val Ala Pro  
 275 280 285  
 Thr Thr Asp Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr  
 290 295 300  
 Asp Gly Ser Met Ala Thr Gly Trp Val Gln Val Asn Ser Ser Trp Tyr  
 305 310 315 320  
 Tyr Leu Asn Ser Asn Gly Ser Met Lys Val Asn Gln Trp Phe Gln Val  
 325 330 335  
 Gly Gly Lys Trp Tyr Tyr Val Asn Thr Ser Gly Glu Leu Ala Val Asn  
 340 345 350  
 Thr Ser Ile Asp Gly Tyr Arg Val Asn Asp Asn Gly Glu Trp Val Arg  
 355 360 365

## (2) INFORMATION FOR SEQ ID NO: 77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

09765272.012201

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGATAATAGA GAAGCATTAA AAACCTTTAT GACGGGTGAA AATTTTATC TCCAACATTA 60  
 TCTAGGAGCA CATAGGGAAG AACTAAATGG AGAGCATGGC TATACCTTCC GTGTTTGGGC 120  
 ACCTAATGCT CAGGCTGTTC ACTTGTTGG TGATTTTACC AACTGGATTG AAAATCAGAT 180  
 TCCAATGGTA AGAAATGATT TTGGGGTCTG GGAAGTCTTT ACCAATATGG CTCAAGAAGG 240  
 GCATATTTAC AAATATCATG TCACACGTCA AAATGGTCAT CAACTGATGA AGATTGACCC 300  
 TTTTGCTGTC AGGTATGAGG CTCGTCCAGG AACAGGGGCA ATCGTAACAG AGCTTCCTGA 360  
 GAAGAAATGG AAGGATGGAC TTTGGCTGGC ACGAAGAAAA CGTTGGGGCT TTGAAGAGCG 420  
 TCCTGTCAAT ATTTATGAAG TTCACGCTGG ATCATGGAAA AGAAATTCTG ATGGCAGTCC 480  
 TTATAGTTTT GCCCAGCTCA AGGATGAACT CATTCTTAT CTCGTTGAAA TGAACATATAC 540  
 TCATATTGAG TTTATGCCCT TGATGTCCCA TCCTTTGGGC TTGAGTTGGG GGTATCAGCT 600  
 TATGGGTTAC TTCGCTTTAG AGCATGCTTA TGGCCGACCA GAGGAGTTTC AAGATTTTGT 660  
 C 661

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asp Asn Arg Glu Ala Leu Lys Thr Phe Met Thr Gly Glu Asn Phe Tyr  
 1 5 10 15  
 Leu Gln His Tyr Leu Gly Ala His Arg Glu Glu Leu Asn Gly Glu His  
 20 25 30  
 Gly Tyr Thr Phe Arg Val Trp Ala Pro Asn Ala Gln Ala Val His Leu  
 35 40 45  
 Val Gly Asp Phe Thr Asn Trp Ile Glu Asn Gln Ile Pro Met Val Arg  
 50 55 60  
 Asn Asp Phe Gly Val Trp Glu Val Phe Thr Asn Met Ala Gln Glu Gly  
 65 70 75 80  
 His Ile Tyr Lys Tyr His Val Thr Arg Gln Asn Gly His Gln Leu Met  
 85 90 95  
 Lys Ile Asp Pro Phe Ala Val Arg Tyr Glu Ala Arg Pro Gly Thr Gly  
 100 105 110  
 Ala Ile Val Thr Glu Leu Pro Glu Lys Lys Trp Lys Asp Gly Leu Trp

09765272 012201  
 102210 2259760

115	120	125
Leu Ala Arg Arg Lys Arg Trp Gly Phe Glu Glu Arg Pro Val Asn Ile		
130	135	140
Tyr Glu Val His Ala Gly Ser Trp Lys Arg Asn Ser Asp Gly Ser Pro		
145	150	155
		160
Tyr Ser Phe Ala Gln Leu Lys Asp Glu Leu Ile Pro Tyr Leu Val Glu		
	165	170
		175
Met Asn Tyr Thr His Ile Glu Phe Met Pro Leu Met Ser His Pro Leu		
	180	185
		190
Gly Leu Ser Trp Gly Tyr Gln Leu Met Gly Tyr Phe Ala Leu Glu His		
	195	200
		205
Ala Tyr Gly Arg Pro Glu Glu Phe Gln Asp Phe Val		
	210	215
		220

## (2) INFORMATION FOR SEQ ID NO: 79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AGATTTTGTGTC GAGGAGTGTGTC ATACCCATAA TATTGGGGTT ATTGTGGACT GGGTACCAGN	60
TCACTTTACC ATCAACGATG ATGCCTTAGC CTATTATGAT GGGACACCGA CTTTGAATA	120
CCAAGACCAT AATAAGGCTC ATAACCATGG TTGGGGTGCC CTTAATTTTG ACCTTGAAAA	180
AAATGAAGTC CAGTCCTTCT TAATTTCTTG CATTAAGCAT TGGATTGATG TCTATCATTT	240
GGATGGTATT CGTGTGGATG CTGTTAGCAA CATGCTCTAT TTGGACTATG ATGATGCTCC	300
ATGGACACCT AATAAAGATG GCGGAAATCT CAACTATGAA GGTTATTATT TCCTTCAGCG	360
CTTGAATGAG GTTATTAAGT TAGAATATCC AGATGTGATG ATGATTGCAG AAGAAAGTTC	420
GTCTGCGATC AAGATTACGG GAATGAAAGA GATTGGTGGT CTAGGATTTG ACTACAAATG	480
GAACATGGGC TGGATGAATG ATATCCTCCG TTTCTACGAA GAAGATCCGA TCTATCGTAA	540
ATATGACTTT AACCTGGTGA CTTTCAGCTT TATGTATGTT TNCAAGGAGA ATTATCTCTT	600
GCCATTCTCG CACGATGAAG TGGTTCATGG CAAGAAGAGT ATGATGCATA AGATGTGGGG	660
AGATCGTTAC AATCAATTCTG CAGGCTTGCG CAATCTCTAT ACGTACCAAA TTTGTCACCC	720
TGGTAAGAAA TTGCTCTTCA TGGGTAGCGA ATACGGTCAA TTCCTAGAAT GGAAATCTGA	780
AGAACAGTTG GAATGGTCTA ACCTAGAAGA CCCAATGAAT GCTAAGATGA AGTATTTTCGC	840
TTCTCAGCTA AACCAGTTTT ACAAAGATCA TCGCTGTCTG TGGGAAATTG ATACCAGCTA	900
TGATGGTATT GAAATCATTG ATGCGGATAA TCGAGACCAG AGTGTCTTT CTTTTATTCTG	960

09765272 "012201



TAAGGGTAAA AAGGGA

976

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Asp Phe Val Glu Glu Cys His Thr His Asn Ile Gly Val Ile Val Asp
1           5           10           15
Trp Val Pro Xaa His Phe Thr Ile Asn Asp Asp Ala Leu Ala Tyr Tyr
          20           25           30
Asp Gly Thr Pro Thr Phe Glu Tyr Gln Asp His Asn Lys Ala His Asn
          35           40           45
His Gly Trp Gly Ala Leu Asn Phe Asp Leu Gly Lys Asn Glu Val Gln
          50           55           60
Ser Phe Leu Ile Ser Cys Ile Lys His Trp Ile Asp Val Tyr His Leu
65           70           75           80
Asp Gly Ile Arg Val Asp Ala Val Ser Asn Met Leu Tyr Leu Asp Tyr
          85           90           95
Asp Asp Ala Pro Trp Thr Pro Asn Lys Asp Gly Gly Asn Leu Asn Tyr
          100          105          110
Glu Gly Tyr Tyr Phe Leu Gln Arg Leu Asn Glu Val Ile Lys Leu Glu
          115          120          125
Tyr Pro Asp Val Met Met Ile Ala Glu Glu Ser Ser Ser Ala Ile Lys
          130          135          140
Ile Thr Gly Met Lys Glu Ile Gly Gly Leu Gly Phe Asp Tyr Lys Trp
          145          150          155          160
Asn Met Gly Trp Met Asn Asp Ile Leu Arg Phe Tyr Glu Glu Asp Pro
          165          170          175
Ile Tyr Arg Lys Tyr Asp Phe Asn Leu Val Thr Phe Ser Phe Met Tyr
          180          185          190
Val Xaa Lys Glu Asn Tyr Leu Leu Pro Phe Ser His Asp Glu Val Val
          195          200          205
His Gly Lys Lys Ser Met Met His Lys Met Trp Gly Asp Arg Tyr Asn
          210          215          220
Gln Phe Ala Gly Leu Arg Asn Leu Tyr Thr Tyr Gln Ile Cys His Pro
          225          230          235          240
Gly Lys Lys Leu Leu Phe Met Gly Ser Glu Tyr Gly Gln Phe Leu Glu
          245          250          255

```

097655272.012201

Trp Lys Ser Glu Glu Gln Leu Glu Trp Ser Asn Leu Glu Asp Pro Met  
 260 265 270  
 Asn Ala Lys Met Lys Tyr Phe Ala Ser Gln Leu Asn Gln Phe Tyr Lys  
 275 280 285  
 Asp His Arg Cys Leu Trp Glu Ile Asp Thr Ser Tyr Asp Gly Ile Glu  
 290 295 300  
 Ile Ile Asp Ala Asp Asn Arg Asp Gln Ser Val Leu Ser Phe Ile Arg  
 305 310 315 320  
 Lys Gly Lys Lys Gly  
 325

## (2) INFORMATION FOR SEQ ID NO: 81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ATCTGTAGTT TATGCGGATG AAACACTTAT TACTCATACT GCTGAGAAAC CTAAAGAGGA 60  
 AAAAATGATA GTAGAAGAAA AGGCTGATAA AGCTTTGGAA ACTAAAAATA TAGTTGAAAG 120  
 GACAGAACAA AGTGAACCTA GTTCAACTGA GGCTATTGCA TCTGAGNAGA AAGAAGATGA 180  
 AGCCGTA ACT CCAAAGAGG AAAAAGTGTC TGCTAAACCG GAAGAAAAAG CTCCAAGGAT 240  
 AGAATCACAA GCTTCAAATC AAGAAAAACC GCTCAAGGAA GATGCTAAAG CTGTAACAAA 300  
 TGAAGAAGTG AATCAAATGA TTGAAGACAG GAAAGTGGAT TTTAATCAAA ATTGGTACTT 360  
 TAAACTCAAT GCAAATTCTA AGGAAGCCAT TAAACCTGAT GCAGACGTAT CTACGTGGAA 420  
 AAAATTAGAT TTACCGTATG ACTGGAGTAT CTTTAACGAT TTCGATCATG AATCTCCTGC 480  
 ACAAATGAA GGTGGACAGC TCAACGGTGG GGAAGCTTGG TATCGCAAGA CTTTCAAAC 540  
 AGATGAAAAA GACCTCAAGA AAAATGTTTCG CCTTACTTTT GATGGCGTCT ACATGGATTC 600  
 TCAAGTTTAT GTCAATGGTC AGTTAGTGGG GCATTATCCA AATGGTTATA ACCAGTTCTC 660  
 ATATGATATC ACCAAATACC TTCAAAAAGA TGGTCGTGAG AATGTGATTG CTGTCCATGC 720  
 AGTCAACAAA CAGCCAAGTA GCCGTTGGTA TTCAGGAAGT GGTATCTATC GTGATGTGAC 780  
 TTTACAAGTG ACAGATAAGG TGCATGTTGA GAAAAATGGG ACAACTATTT TAACACCAAA 840  
 ACTTGAAGAA CAACAACATG GCAAGGTTGA AACTCATGTG ACCAGCAAAA TCGTCAATAC 900  
 GGACGACAAA GACCATGAAC TTGTAGCCGA ATATCAAATC GTTGAACGAG GTGGTCATGC 960  
 TGTAACAGGC TTAGTTCGTA CAGCGAGTCG TACCTTAAAA GCACATGAAT CAACAAGCCT 1020  
 AGATGCGATT TTAGAAGTTG AAAGACCAAA ACTCTGGACT GTTTTAAATG ACAAACCTGC 1080

09765272.012201

(2) INFORMATION FOR SEQ ID NO:82:

(A) LENGTH: 711 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Lys Glu Glu Lys Val Ser Ala Lys Pro Glu Glu Lys Ala Pro Arg Ile

65					70						75				80
Glu	Ser	Gln	Ala	Ser	Asn	Gln	Glu	Lys	Pro	Leu	Lys	Glu	Asp	Ala	Lys
				85					90					95	
Ala	Val	Thr	Asn	Glu	Glu	Val	Asn	Gln	Met	Ile	Glu	Asp	Arg	Lys	Val
			100					105					110		
Asp	Phe	Asn	Gln	Asn	Trp	Tyr	Phe	Lys	Leu	Asn	Ala	Asn	Ser	Lys	Glu
		115					120					125			
Ala	Ile	Lys	Pro	Asp	Ala	Asp	Val	Ser	Thr	Trp	Lys	Lys	Leu	Asp	Leu
	130					135					140				
Pro	Tyr	Asp	Trp	Ser	Ile	Phe	Asn	Asp	Phe	Asp	His	Glu	Ser	Pro	Ala
145					150					155					160
Gln	Asn	Glu	Gly	Gly	Gln	Leu	Asn	Gly	Gly	Glu	Ala	Trp	Tyr	Arg	Lys
			165						170					175	
Thr	Phe	Lys	Leu	Asp	Glu	Lys	Asp	Leu	Lys	Lys	Asn	Val	Arg	Leu	Thr
			180					185					190		
Phe	Asp	Gly	Val	Tyr	Met	Asp	Ser	Gln	Val	Tyr	Val	Asn	Gly	Gln	Leu
	195						200					205			
Val	Gly	His	Tyr	Pro	Asn	Gly	Tyr	Asn	Gln	Phe	Ser	Tyr	Asp	Ile	Thr
	210					215					220				
Lys	Tyr	Leu	Gln	Lys	Asp	Gly	Arg	Glu	Asn	Val	Ile	Ala	Val	His	Ala
225					230					235					240
Val	Asn	Lys	Gln	Pro	Ser	Ser	Arg	Trp	Tyr	Ser	Gly	Ser	Gly	Ile	Tyr
				245					250					255	
Arg	Asp	Val	Thr	Leu	Gln	Val	Thr	Asp	Lys	Val	His	Val	Glu	Lys	Asn
		260						265					270		
Gly	Thr	Thr	Ile	Leu	Thr	Pro	Lys	Leu	Glu	Glu	Gln	Gln	His	Gly	Lys
		275					280					285			
Val	Glu	Thr	His	Val	Thr	Ser	Lys	Ile	Val	Asn	Thr	Asp	Asp	Lys	Asp
	290					295					300				
His	Glu	Leu	Val	Ala	Glu	Tyr	Gln	Ile	Val	Glu	Arg	Gly	Gly	His	Ala
305					310					315					320
Val	Thr	Gly	Leu	Val	Arg	Thr	Ala	Ser	Arg	Thr	Leu	Lys	Ala	His	Glu
			325						330					335	
Ser	Thr	Ser	Leu	Asp	Ala	Ile	Leu	Glu	Val	Glu	Arg	Pro	Lys	Leu	Trp
			340					345					350		
Thr	Val	Leu	Asn	Asp	Lys	Pro	Ala	Leu	Tyr	Glu	Leu	Ile	Thr	Arg	Val
		355					360					365			
Tyr	Arg	Asp	Gly	Gln	Leu	Val	Asp	Ala	Lys	Lys	Asp	Leu	Phe	Gly	Tyr
	370					375					380				
Arg	Tyr	Tyr	His	Trp	Thr	Pro	Asn	Glu	Gly	Phe	Ser	Leu	Asn	Gly	Glu
385						390				395					400
Arg	Ile	Lys	Phe	His	Gly	Val	Ser	Leu	His	His	Asp	His	Gly	Ala	Leu

09765272-0122004

405

410

415

Gly Ala Glu Glu Asn Tyr Lys Ala Glu Tyr Arg Arg Leu Lys Gln Met  
 420 425 430  
 Lys Glu Met Gly Val Asn Ser Ile Arg Thr Thr His Asn Pro Ala Ser  
 435 440 445  
 Glu Gln Thr Leu Gln Ile Ala Ala Glu Leu Gly Leu Leu Val Gln Glu  
 450 455 460  
 Glu Ala Phe Asp Thr Trp Tyr Gly Gly Lys Lys Pro Tyr Asp Tyr Gly  
 465 470 475 480  
 Arg Phe Phe Glu Lys Asp Ala Thr His Pro Glu Ala Arg Lys Gly Glu  
 485 490 495  
 Lys Trp Ser Asp Phe Asp Leu Arg Thr Met Val Glu Arg Gly Lys Asn  
 500 505 510  
 Asn Pro Ala Ile Phe Met Trp Ser Ile Gly Asn Glu Ile Gly Glu Ala  
 515 520 525  
 Asn Gly Asp Ala His Ser Leu Ala Thr Val Lys Arg Leu Val Lys Val  
 530 535 540  
 Ile Lys Asp Val Asp Lys Thr Arg Tyr Val Thr Met Gly Ala Asp Lys  
 545 550 555 560  
 Phe Arg Phe Gly Asn Gly Ser Gly Gly His Glu Lys Ile Ala Asp Glu  
 565 570 575  
 Leu Asp Ala Val Gly Phe Asn Tyr Ser Glu Asp Asn Tyr Lys Ala Leu  
 580 585 590  
 Arg Ala Lys His Pro Lys Trp Leu Ile Tyr Gly Ser Glu Thr Ser Ser  
 595 600 605  
 Ala Thr Arg Thr Arg Gly Ser Tyr Tyr Arg Pro Glu Arg Glu Leu Lys  
 610 615 620  
 His Ser Asn Gly Pro Glu Arg Asn Tyr Glu Gln Ser Asp Tyr Gly Asn  
 625 630 635 640  
 Asp Arg Val Gly Trp Gly Lys Thr Ala Thr Ala Ser Trp Thr Phe Asp  
 645 650 655  
 Arg Asp Asn Ala Gly Tyr Ala Gly Gln Phe Ile Trp Thr Gly Thr Asp  
 660 665 670  
 Tyr Ile Gly Glu Pro Thr Pro Trp His Asn Gln Asn Gln Thr Pro Val  
 675 680 685  
 Lys Ser Ser Tyr Phe Gly Ile Val Asp Thr Ala Gly Ile Pro Lys His  
 690 695 700  
 Asp Phe Tyr Leu Tyr Gln Ser  
 705 710

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2167 base pairs

00766672.012201

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTACTTTGGT ATCGTAGATA CAGCCGGCAT TCCAAAACAT GACTTCTATC TCTACCAAAG	60
CCAATGGGTT TCTGTTAAGA AGAAACCGAT GGTACACCTT CTTCTCACT GGAAGTGGGA	120
AAACAAAGAA TTAGCATCCA AAGTAGCTGA CTCAGAAGGT AAGATTCCAG TTCGTGCTTA	180
TTCGAATGCT TCTAGTGTAG AATTGTTCTT GAATGGAAAA TCTCTTGGTC TTAAGACTTT	240
CAATAAAAAA CAAACCAGCG ATGGGCGGAC TTACCAAGAA GGTGCAAATG CTAATGAACT	300
TTATCTTGAA TGGAAAGTTG CCTATCAACC AGGTACCTTG GAAGCAATTG CTCGTGATGA	360
ATCTGGCAAG GAAATTGCTC GAGATAAGAT TACGACTGCT GGTAAGCCAG CGGCAGTTCTG	420
TCTTATTAAG GAAGACCATG CGATTGCAGC AGATGGAAAA GACTTGACTT ACATCTACTA	480
TGAAATTGTT GACAGCCAGG GGAATGTGGT TCCAACCTGCT AATAATCTGG TTCGCTTCCA	540
ATTGCATGGC CAAGGTCAAC TGGTCGGTGT AGATAACGGA GAACAAGCCA GCCGTGAACG	600
CTATAAGGCG CAAGCAGATG GTTCTTGGAT TCGTAAAGCA TTTAATGGTA AAGGTGTTGC	660
CATTGTCAAA TCAACTGAAC AAGCAGGGAA ATTCACCCTG ACTGCCCCACT CTGATCTCTT	720
GAAATCGAAC CAAGTCACTG TCTTTACTGG TAAGAAAGAA GGACAAGAGA AGACTGTTTT	780
GGGGACAGAA GTGCCAAAAG TACAGACCAT TATTGGAGAG GCACCTGAAA TGCCTACCAC	840
TGTTCCGTTT GTATACAGTG ATGGTAGCCG TGCAGAACGT CCTGTAACCT GGTCTTCAGT	900
AGATGTGAGC AAGCCTGGTA TTGTAACGGT GAAAGGTATG GCTGACGGAC GAGAAGTAGA	960
AGCTCGTGTA GAAGTGATTG CTCTTAAATC AGAGCTACCA GTTGTGAAAC GTATTGCTCC	1020
AAATACTGAC TTGAATTCTG TAGACAAATC TGTTTCCTAT GTTTTGATTG ATGGAAGTGT	1080
TGAAGAGTAT GAAGTGGACA AGTGGGAGAT TGCCGAAGAA GATAAAGCTA AGTTAGCAAT	1140
TCCAGGTTCT CGTATTCAAG CGACCGGTTA TTTAGAAGGT CAACCAATTC ATGCAACCCCT	1200
TGTGGTAGAA GAAGGCAATC CTGCGGCACC TGCAGTACCA ACTGTAACGG TTGGTGGTGA	1260
GGCAGTAACA GGTCTTACTA GTCAAAAACC AATGCAATAC CGCACTCTTG CTTATGGAGC	1320
TAAGTTGCCA GAAGTCACAG CAAGTGCTAA AAATGCAGCT GTTACAGTTC TTCAAGCAAG	1380
CGCAGCAAAC GGCATGCGTG CGAGCATCTT TATTCAGCCT AAAGATGGTG GCCCTCTTCA	1440
AACCTATGCA ATTCAATTCC TTGAAGAAGC GCCAAAAATT GCTCACTTGA GCTTGCAAGT	1500
GGAAAAAGCT GACAGTCTCA AAGAAGACCA AACTGTCAAA TTGTCGGTTC GAGCTCACTA	1560
TCAAGATGGA ACGCAAGCTG TATTACCAGC TGATAAAGTA ACCTTCTCTA CAAGTGGTGA	1620
AGGGGAAGTC GCAATTGCGTA AAGGAATGCT TGAGTTGCAT AAGCCAGGAG CAGTCACTCT	1680

09765272.012201

GAACGCTGAA TATGAGGGAG CTAAAGACCA AGTTGAACTC ACTATCCAAG CCAATACTGA 1740  
 GAAGAAGATT GCGCAATCCA TCCGTCCTGT AAATGTAGTG ACAGATTTGC ATCAGGAACC 1800  
 AAGTCTTCCA GCAACAGTAA CAGTTGAGTA TGACAAAGGT TTCCCTAAAA CTCATAAAGT 1860  
 CACTTGCGAA GCTATTCCGA AAGAAAAACT AGACTCCTAT CAAACATTTG AAGTACTAGG 1920  
 TAAAGTTGAA GGAATTGACC TTGAAGCGCG TGCAAAAGTC TCTGTAGAAG GTATCGTTTC 1980  
 AGTTGAAGAA GTCAGTGTGA CAACTCCAAT CGCAGAAGCA CCACAATTAC CAGAAAGTGT 2040  
 TCGGACATAT GATTCAAATG GTCACGTTTC ATCAGCTAAG GTTGCATGGG ATGCGATTTCG 2100  
 TCCAGAGCAA TACGCTAAGG AAGGTGTCTT TACAGTTAAT GGTCGCTTAG AAGGTACGCA 2160  
 ATTAACA 2167

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr	Phe	Gly	Ile	Val	Asp	Thr	Ala	Gly	Ile	Pro	Lys	His	Asp	Phe	Tyr
1				5					10					15	
Leu	Tyr	Gln	Ser	Gln	Trp	Val	Ser	Val	Lys	Lys	Lys	Pro	Met	Val	His
			20					25					30		
Leu	Leu	Pro	His	Trp	Asn	Trp	Glu	Asn	Lys	Glu	Leu	Ala	Ser	Lys	Val
		35					40					45			
Ala	Asp	Ser	Glu	Gly	Lys	Ile	Pro	Val	Arg	Ala	Tyr	Ser	Asn	Ala	Ser
	50					55					60				
Ser	Val	Glu	Leu	Phe	Leu	Asn	Gly	Lys	Ser	Leu	Gly	Leu	Lys	Thr	Phe
65				70					75					80	
Asn	Lys	Lys	Gln	Thr	Ser	Asp	Gly	Arg	Thr	Tyr	Gln	Glu	Gly	Ala	Asn
			85					90						95	
Ala	Asn	Glu	Leu	Tyr	Leu	Glu	Trp	Lys	Val	Ala	Tyr	Gln	Pro	Gly	Thr
		100					105						110		
Leu	Glu	Ala	Ile	Ala	Arg	Asp	Glu	Ser	Gly	Lys	Glu	Ile	Ala	Arg	Asp
	115						120					125			
Lys	Ile	Thr	Thr	Ala	Gly	Lys	Pro	Ala	Ala	Val	Arg	Leu	Ile	Lys	Glu
	130					135					140				
Asp	His	Ala	Ile	Ala	Ala	Asp	Gly	Lys	Asp	Leu	Thr	Tyr	Ile	Tyr	Tyr
145				150					155					160	
Glu	Ile	Val	Asp	Ser	Gln	Gly	Asn	Val	Val	Pro	Thr	Ala	Asn	Asn	Leu

097655272.012201

165										170				175			
Val	Arg	Phe	Gln	Leu	His	Gly	Gln	Gly	Gln	Leu	Val	Gly	Val	Asp	Asn		
			180						185				190				
Gly	Glu	Gln	Ala	Ser	Arg	Glu	Arg	Tyr	Lys	Ala	Gln	Ala	Asp	Gly	Ser		
		195					200					205					
Trp	Ile	Arg	Lys	Ala	Phe	Asn	Gly	Lys	Gly	Val	Ala	Ile	Val	Lys	Ser		
	210					215					220						
Thr	Glu	Gln	Ala	Gly	Lys	Phe	Thr	Leu	Thr	Ala	His	Ser	Asp	Leu	Leu		
225					230					235					240		
Lys	Ser	Asn	Gln	Val	Thr	Val	Phe	Thr	Gly	Lys	Lys	Glu	Gly	Gln	Glu		
				245					250					255			
Lys	Thr	Val	Leu	Gly	Thr	Glu	Val	Pro	Lys	Val	Gln	Thr	Ile	Ile	Gly		
			260					265					270				
Glu	Ala	Pro	Glu	Met	Pro	Thr	Thr	Val	Pro	Phe	Val	Tyr	Ser	Asp	Gly		
		275					280					285					
Ser	Arg	Ala	Glu	Arg	Pro	Val	Thr	Trp	Ser	Ser	Val	Asp	Val	Ser	Lys		
	290					295					300						
Pro	Gly	Ile	Val	Thr	Val	Lys	Gly	Met	Ala	Asp	Gly	Arg	Glu	Val	Glu		
305					310					315					320		
Ala	Arg	Val	Glu	Val	Ile	Ala	Leu	Lys	Ser	Glu	Leu	Pro	Val	Val	Lys		
				325					330					335			
Arg	Ile	Ala	Pro	Asn	Thr	Asp	Leu	Asn	Ser	Val	Asp	Lys	Ser	Val	Ser		
			340					345					350				
Tyr	Val	Leu	Ile	Asp	Gly	Ser	Val	Glu	Glu	Tyr	Glu	Val	Asp	Lys	Trp		
		355					360					365					
Glu	Ile	Ala	Glu	Glu	Asp	Lys	Ala	Lys	Leu	Ala	Ile	Pro	Gly	Ser	Arg		
	370					375					380						
Ile	Gln	Ala	Thr	Gly	Tyr	Leu	Glu	Gly	Gln	Pro	Ile	His	Ala	Thr	Leu		
385					390					395					400		
Val	Val	Glu	Glu	Gly	Asn	Pro	Ala	Ala	Pro	Ala	Val	Pro	Thr	Val	Thr		
				405					410					415			
Val	Gly	Gly	Glu	Ala	Val	Thr	Gly	Leu	Thr	Ser	Gln	Lys	Pro	Met	Gln		
			420					425					430				
Tyr	Arg	Thr	Leu	Ala	Tyr	Gly	Ala	Lys	Leu	Pro	Glu	Val	Thr	Ala	Ser		
		435					440					445					
Ala	Lys	Asn	Ala	Ala	Val	Thr	Val	Leu	Gln	Ala	Ser	Ala	Ala	Asn	Gly		
	450					455					460						
Met	Arg	Ala	Ser	Ile	Phe	Ile	Gln	Pro	Lys	Asp	Gly	Gly	Pro	Leu	Gln		
465					470					475					480		
Thr	Tyr	Ala	Ile	Gln	Phe	Leu	Glu	Glu	Ala	Pro	Lys	Ile	Ala	His	Leu		
				485					490					495			
Ser	Leu	Gln	Val	Glu	Lys	Ala	Asp	Ser	Leu	Lys	Glu	Asp	Gln	Thr	Val		



202

500

505

510

Lys Leu Ser Val Arg Ala His Tyr Gln Asp Gly Thr Gln Ala Val Leu  
 515 520 525  
 Pro Ala Asp Lys Val Thr Phe Ser Thr Ser Gly Glu Gly Glu Val Ala  
 530 535 540  
 Ile Arg Lys Gly Met Leu Glu Leu His Lys Pro Gly Ala Val Thr Leu  
 545 550 555 560  
 Asn Ala Glu Tyr Glu Gly Ala Lys Asp Gln Val Glu Leu Thr Ile Gln  
 565 570 575  
 Ala Asn Thr Glu Lys Lys Ile Ala Gln Ser Ile Arg Pro Val Asn Val  
 580 585 590  
 Val Thr Asp Leu His Gln Glu Pro Ser Leu Pro Ala Thr Val Thr Val  
 595 600 605  
 Glu Tyr Asp Lys Gly Phe Pro Lys Thr His Lys Val Thr Trp Gln Ala  
 610 615 620  
 Ile Pro Lys Glu Lys Leu Asp Ser Tyr Gln Thr Phe Glu Val Leu Gly  
 625 630 635 640  
 Lys Val Glu Gly Ile Asp Leu Glu Ala Arg Ala Lys Val Ser Val Glu  
 645 650 655  
 Gly Ile Val Ser Val Glu Glu Val Ser Val Thr Thr Pro Ile Ala Glu  
 660 665 670  
 Ala Pro Gln Leu Pro Glu Ser Val Arg Thr Tyr Asp Ser Asn Gly His  
 675 680 685  
 Val Ser Ser Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr  
 690 695 700  
 Ala Lys Glu Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln  
 705 710 715 720  
 Leu Thr

## (2) INFORMATION FOR SEQ ID NO: 85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AGCTAAGGTT GCATGGGATG CGATTTCGTCC AGAGCAATAC GCTAAGGAAG GTGTCTTTAC	60
AGTTAATGGT CGCTTAGAAG GTACGCAATT AACAACTAAA CTTTCATGTTT CCGTATCTGC	120
TCAAACCTGAG CAAGGTGCAA ACATTTCTGA CCAATGGACC GGTTCAGAAT TGCCACTTGC	180
CTTTGCTTCA GACTCAAATC CAAGCGACCC AGTTTCAAAT GTTAATGACA AGCTCATTTT	240

097655272.012201

CTACAATAAC	CAACCAGCCA	ATCGTTGGAC	AAACTGGAAT	CGTACTAATC	CAGAAGCTTC	300
AGTCGGTGTT	CTGTTTGGAG	ATTCAGGTAT	CTTGAGCAAA	CGCTCCGTTG	ATAATCTAAG	360
TGTCGGATTG	CATGAAGACC	ATGGAGTTGG	TGTACCGAAG	TCTTATGTGA	TTGAGTATTA	420
TGTTGGTAAG	ACTGTCCCAA	CAGCTCCTAA	AAACCCTAGT	TTTGTGGTA	ATGAGGACCA	480
TGTCTTTAAT	GATTCTGCCA	ACTGGAAACC	AGTTACTAAT	CTAAAAGCCC	CTGCTCAACT	540
CAAGGCTGGA	GAAATGAACC	ACTTTAGCTT	TGATAAAGTT	GAAACCTATG	CTGTTTCGTAT	600
TCGCATGGTT	AAAGCAGATA	ACAAGCGTGG	AACGTCTATC	ACAGAGGTAC	AAATCTTTGC	660
GAAACAAGTT	GCGGCAGCCA	AGCAAGGACA	AACAAGAATC	CAAGTTGACG	GCAAAGACTT	720
AGCAAAC TTC	AACCCTGATT	TGACAGACTA	CTACCTTGAG	TCTGTAGATG	GAAAAGTTCC	780
GGCAGTCACA	GCAAGTGTTA	GCAACAATGG	TCTCGCTACC	GTCGTTCCAA	GCGTTTCGTGA	840
AGGTGAGCCA	GTTTCGTGTCA	TCGCGAAAGC	TGAAAATGGC	GACATCTTAG	GAGAATACCG	900
TCTGCACTTC	ACTAAGGATA	AGAGCTTACT	TTCTCATAAA	CCAGTTGCTG	CGGTAAACA	960
AGCTCGCTTG	CTACAAGTAG	GTCAAGCACT	TGAATTGCCG	ACTAAGGTTT	CAGTTTACTT	1020
CACAGGTAAG	GACGGCTACG	AAACAAAAGA	CCTGACAGTT	GAATGGGAAG	AAGTTCCAGC	1080
GGAAAATCTG	ACAAAAGCAG	GTCAATTTAC	TGTTTCGAGGC	CGTGTCTTGG	GTAAGTAACCT	1140
TGTTGCTGAG	ATCACTGTAC	GAGTGACAGA	CAAACCTGGT	GAGACTCTTT	CAGATAACCC	1200
TAACATGAT	GAAAACAGTA	ACCAGGCCTT	TGCTTCAGCA	ACCAATGATA	TTGACAAAAA	1260
CTCTCATGAC	CGCGTTGACT	ATCTCAATGA	CGGAGATCAT	TCAGAAAATC	GTCGTTGGAC	1320
AAACTGGTCA	CCAACACCAT	CTTCTAATCC	AGAAGTATCA	GCGGGTGTGA	TTTTCCGTGA	1380
AAATGGTAAG	ATTGTAGAAC	GGACTGTTAC	ACAAGGAAAA	GTTTCAGTTCT	TTGCAGATAG	1440
TGGTACGGAT	GCACCATCTA	AACCTGTTTT	AGAACGCTAT	GTCGGTCCAG	AGTTTGAAGT	1500
GCCAACCTAC	TATTCAAAC	ACCAAGCCTA	CGACGCAGAC	CATCCATTCA	ACAATCCAGA	1560
AAATGGGAA	GCTGTTTCCT	ATCGTGCGGA	TAAAGACATT	GCAGCTGGTG	ATGAAATCAA	1620
CGTAACATTT	AAAGCTATCA	AAGCCAAAGC	TATGAGATGG	CGTATGGAGC	GTAAAGCAGA	1680
TAAGAGCGGT	GTTGCGATGA	TTGAGATGAC	CTTCCTTGCA	CCAAGTGAAT	TGCCTCAAGA	1740
AAGCACTCAA	TCAAAGATTG	TTGTAGATGG	AAAAGAAGTT	GCTGATTTTCG	CTGAAAATCG	1800
TCAAGACTAT	CAAATTACCT	ATAAAGGTCA	ACGGCCAAAA	GTCTCAGTTG	AAGAAAACAA	1860
TCAAGTAGCT	TCAACTGTGG	TAGATAGTGG	AGAAGATAGC	TTTCCAGTAC	TTGTTCGCCT	1920
CGTTTCAGAA	AGTGGAAAAC	AAGTCAAGGA	ATACCGTATC	CACCTGACTA	AGGAAAAACC	1980
AGTTTCTGAG	AAGACAGTTG	CTGCTGTACA	AGAAGATCTT	CCAAAAATCG	AATTTGTTGA	2040
AAAAGATTTG	GCATACAAGA	CAGTTGAGAA	AAAAGATTCA	ACACTGTATC	TAGGTGAAAC	2100

TCGTGTAGAA CAAGAAGGAA AAGTTGGAAA AGAACGTATC TTTACAGCGA TTAATCCTGA 2160  
 TGGAAGTAAG GAAGAAAAAC TCCGTGAAGT GGTAGAAGTT CCGACAGACC GCATCGTCTT 2220  
 GGTGGAACC AAACAGTAG CTCAAGAAGC TAAAAAACCA CAAGTGTCAG AAAAAGCAGA 2280  
 TACAAAACCA ATTGATTCAA GTGAAGCTAG TCAAATAAT AAAGCCCAG 2329

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ala Lys Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr Ala Lys Glu  
 1 5 10 15  
 Gly Val Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln Leu Thr Thr  
 20 25 30  
 Lys Leu His Val Arg Val Ser Ala Gln Thr Glu Gln Gly Ala Asn Ile  
 35 40 45  
 Ser Asp Gln Trp Thr Gly Ser Glu Leu Pro Leu Ala Phe Ala Ser Asp  
 50 55 60  
 Ser Asn Pro Ser Asp Pro Val Ser Asn Val Asn Asp Lys Leu Ile Ser  
 65 70 75 80  
 Tyr Asn Asn Gln Pro Ala Asn Arg Trp Thr Asn Trp Asn Arg Thr Asn  
 85 90 95  
 Pro Glu Ala Ser Val Gly Val Leu Phe Gly Asp Ser Gly Ile Leu Ser  
 100 105 110  
 Lys Arg Ser Val Asp Asn Leu Ser Val Gly Phe His Glu Asp His Gly  
 115 120 125  
 Val Gly Val Pro Lys Ser Tyr Val Ile Glu Tyr Tyr Val Gly Lys Thr  
 130 135 140  
 Val Pro Thr Ala Pro Lys Asn Pro Ser Phe Val Gly Asn Glu Asp His  
 145 150 155 160  
 Val Phe Asn Asp Ser Ala Asn Trp Lys Pro Val Thr Asn Leu Lys Ala  
 165 170 175  
 Pro Ala Gln Leu Lys Ala Gly Glu Met Asn His Phe Ser Phe Asp Lys  
 180 185 190  
 Val Glu Thr Tyr Ala Val Arg Ile Arg Met Val Lys Ala Asp Asn Lys  
 195 200 205  
 Arg Gly Thr Ser Ile Thr Glu Val Gln Ile Phe Ala Lys Gln Val Ala  
 210 215 220

09765272.012201

Ala	Ala	Lys	Gln	Gly	Gln	Thr	Arg	Ile	Gln	Val	Asp	Gly	Lys	Asp	Leu	225	230	235	240
Ala	Asn	Phe	Asn	Pro	Asp	Leu	Thr	Asp	Tyr	Tyr	Leu	Glu	Ser	Val	Asp	245	250	255	
Gly	Lys	Val	Pro	Ala	Val	Thr	Ala	Ser	Val	Ser	Asn	Asn	Gly	Leu	Ala	260	265	270	
Thr	Val	Val	Pro	Ser	Val	Arg	Glu	Gly	Glu	Pro	Val	Arg	Val	Ile	Ala	275	280	285	
Lys	Ala	Glu	Asn	Gly	Asp	Ile	Leu	Gly	Glu	Tyr	Arg	Leu	His	Phe	Thr	290	295	300	
Lys	Asp	Lys	Ser	Leu	Leu	Ser	His	Lys	Pro	Val	Ala	Ala	Val	Lys	Gln	305	310	315	320
Ala	Arg	Leu	Leu	Gln	Val	Gly	Gln	Ala	Leu	Glu	Leu	Pro	Thr	Lys	Val	325	330	335	
Pro	Val	Tyr	Phe	Thr	Gly	Lys	Asp	Gly	Tyr	Glu	Thr	Lys	Asp	Leu	Thr	340	345	350	
Val	Glu	Trp	Glu	Glu	Val	Pro	Ala	Glu	Asn	Leu	Thr	Lys	Ala	Gly	Gln	355	360	365	
Phe	Thr	Val	Arg	Gly	Arg	Val	Leu	Gly	Ser	Asn	Leu	Val	Ala	Glu	Ile	370	375	380	
Thr	Val	Arg	Val	Thr	Asp	Lys	Leu	Gly	Glu	Thr	Leu	Ser	Asp	Asn	Pro	385	390	395	400
Asn	Tyr	Asp	Glu	Asn	Ser	Asn	Gln	Ala	Phe	Ala	Ser	Ala	Thr	Asn	Asp	405	410	415	
Ile	Asp	Lys	Asn	Ser	His	Asp	Arg	Val	Asp	Tyr	Leu	Asn	Asp	Gly	Asp	420	425	430	
His	Ser	Glu	Asn	Arg	Arg	Trp	Thr	Asn	Trp	Ser	Pro	Thr	Pro	Ser	Ser	435	440	445	
Asn	Pro	Glu	Val	Ser	Ala	Gly	Val	Ile	Phe	Arg	Glu	Asn	Gly	Lys	Ile	450	455	460	
Val	Glu	Arg	Thr	Val	Thr	Gln	Gly	Lys	Val	Gln	Phe	Phe	Ala	Asp	Ser	465	470	475	480
Gly	Thr	Asp	Ala	Pro	Ser	Lys	Leu	Val	Leu	Glu	Arg	Tyr	Val	Gly	Pro	485	490	495	
Glu	Phe	Glu	Val	Pro	Thr	Tyr	Tyr	Ser	Asn	Tyr	Gln	Ala	Tyr	Asp	Ala	500	505	510	
Asp	His	Pro	Phe	Asn	Asn	Pro	Glu	Asn	Trp	Glu	Ala	Val	Pro	Tyr	Arg	515	520	525	
Ala	Asp	Lys	Asp	Ile	Ala	Ala	Gly	Asp	Glu	Ile	Asn	Val	Thr	Phe	Lys	530	535	540	
Ala	Ile	Lys	Ala	Lys	Ala	Met	Arg	Trp	Arg	Met	Glu	Arg	Lys	Ala	Asp	545	550	555	560

09765272.012201

Lys Ser Gly Val Ala Met Ile Glu Met Thr Phe Leu Ala Pro Ser Glu  
 565 570 575  
 Leu Pro Gln Glu Ser Thr Gln Ser Lys Ile Leu Val Asp Gly Lys Glu  
 580 585 590  
 Leu Ala Asp Phe Ala Glu Asn Arg Gln Asp Tyr Gln Ile Thr Tyr Lys  
 595 600 605  
 Gly Gln Arg Pro Lys Val Ser Val Glu Glu Asn Asn Gln Val Ala Ser  
 610 615 620  
 Thr Val Val Asp Ser Gly Glu Asp Ser Phe Pro Val Leu Val Arg Leu  
 625 630 635 640  
 Val Ser Glu Ser Gly Lys Gln Val Lys Glu Tyr Arg Ile His Leu Thr  
 645 650 655  
 Lys Glu Lys Pro Val Ser Glu Lys Thr Val Ala Ala Val Gln Glu Asp  
 660 665 670  
 Leu Pro Lys Ile Glu Phe Val Glu Lys Asp Leu Ala Tyr Lys Thr Val  
 675 680 685  
 Glu Lys Lys Asp Ser Thr Leu Tyr Leu Gly Glu Thr Arg Val Glu Gln  
 690 695 700  
 Glu Gly Lys Val Gly Lys Glu Arg Ile Phe Thr Ala Ile Asn Pro Asp  
 705 710 715 720  
 Gly Ser Lys Glu Glu Lys Leu Arg Glu Val Val Glu Val Pro Thr Asp  
 725 730 735  
 Arg Ile Val Leu Val Gly Thr Lys Pro Val Ala Gln Glu Ala Lys Lys  
 740 745 750  
 Pro Gln Val Ser Glu Lys Ala Asp Thr Lys Pro Ile Asp Ser Ser Glu  
 755 760 765  
 Ala Ser Gln Thr Asn Lys Ala Gln  
 770 775

## (2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTATCACTAT GTAAATAAAG AGATTATTTT ACAAGAAGCT AAAGATTTAA TTCAGACAGG	60
AAAGCCTGAC AGGAATGAAG TTGTATATGG TTTGGTGTAT CAAAAGATC AGTTGCCTCA	120
AACAGGGACA GAA	133

## (2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:

097655272.012201

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Tyr His Tyr Val Asn Lys Glu Ile Ile Ser Gln Glu Ala Lys Asp Leu
1          5          10          15
Ile Gln Thr Gly Lys Pro Asp Arg Asn Glu Val Val Tyr Gly Leu Val
          20          25          30
Tyr Gln Lys Asp Gln Leu Pro Gln Thr Gly Thr Glu
          35          40

```

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

TGAGACTCCT CAATCAATAA CAAATCAGGA GCAAGCTAGG ACAGAAAACC AAGTAGTAGA      60
GACAGAGGAA GCTCCAAAAG AAGAAGCACC TAAACAGAA GAAAGTCCAA AGGAAGAACC      120
AAAATCGGAG GTAAAACCTA CTGACGACAC CCTTCCTAAA GTAGAAGAGG GGAAAGAAGA      180
TTCAGCAGAA CCAGCTCCAG TTGAAGAAGT AGGTGGAGAA GTTGAGTCAA AACCAGAGGA      240
AAAAGTAGCA GTTAAGCCAG AAAGTCAACC ATCAGACAAA CCAGCTGAGG AATCAAAAGT      300
TGAACAAGCA GGTGAACCAG TCGCGCCAAG AGAAGACGAA AAGGCACCAG TCGAGCCAGA      360
AAAGCAACCA GAAGCTCCTG AAGAAGAGAA GGCTGTAGAG GAAACACCGA AACAGAAGA      420
GTCAACTCCA GATACCAAGG CTGAAGAAAC TGTAGAACCA AAAGAGGAGA CTGTTAATCA      480
ATCTATTGAA CAACCAAAAG TTGAAACGCC TGCTGTAGAA AAACAAACAG AACCAACAGA      540
GGAACCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AACAGGCACC      600
AACGGCACCA GTTGAGCCAG AAAAGCAACC AGAAGTTCCT GAAGAAGAGA AGGCTGTAGA      660
GGAAACACCG AAACCAGAAG ATAAATAAAA GGGTATTGGT ACTAAAGAAC CAGTTGATAA      720
AAGTGAGTTA AATAATCAAA TTGATAAAGC TAGTTCAGTT TCTCCTACTG ATTAT          775

```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

09765272.012201

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Glu	Thr	Pro	Gln	Ser	Ile	Thr	Asn	Gln	Glu	Gln	Ala	Arg	Thr	Glu	Asn	1	5	10	15
Gln	Val	Val	Glu	Thr	Glu	Glu	Ala	Pro	Lys	Glu	Glu	Ala	Pro	Lys	Thr	20	25	30	
Glu	Glu	Ser	Pro	Lys	Glu	Glu	Pro	Lys	Ser	Glu	Val	Lys	Pro	Thr	Asp	35	40	45	
Asp	Thr	Leu	Pro	Lys	Val	Glu	Glu	Gly	Lys	Glu	Asp	Ser	Ala	Glu	Pro	50	55	60	
Ala	Pro	Val	Glu	Glu	Val	Gly	Gly	Glu	Val	Glu	Ser	Lys	Pro	Glu	Glu	65	70	75	80
Lys	Val	Ala	Val	Lys	Pro	Glu	Ser	Gln	Pro	Ser	Asp	Lys	Pro	Ala	Glu	85	90	95	
Glu	Ser	Lys	Val	Glu	Gln	Ala	Gly	Glu	Pro	Val	Ala	Pro	Arg	Glu	Asp	100	105	110	
Glu	Lys	Ala	Pro	Val	Glu	Pro	Glu	Lys	Gln	Pro	Glu	Ala	Pro	Glu	Glu	115	120	125	
Glu	Lys	Ala	Val	Glu	Glu	Thr	Pro	Lys	Gln	Glu	Glu	Ser	Thr	Pro	Asp	130	135	140	
Thr	Lys	Ala	Glu	Glu	Thr	Val	Glu	Pro	Lys	Glu	Glu	Thr	Val	Asn	Gln	145	150	155	160
Ser	Ile	Glu	Gln	Pro	Lys	Val	Glu	Thr	Pro	Ala	Val	Glu	Lys	Gln	Thr	165	170	175	
Glu	Pro	Thr	Glu	Glu	Pro	Lys	Val	Glu	Gln	Ala	Gly	Glu	Pro	Val	Ala	180	185	190	
Pro	Arg	Glu	Asp	Glu	Gln	Ala	Pro	Thr	Ala	Pro	Val	Glu	Pro	Glu	Lys	195	200	205	
Gln	Pro	Glu	Val	Pro	Glu	Glu	Glu	Lys	Ala	Val	Glu	Glu	Thr	Pro	Lys	210	215	220	
Pro	Glu	Asp	Lys	Ile	Lys	Gly	Ile	Gly	Thr	Lys	Glu	Pro	Val	Asp	Lys	225	230	235	240
Ser	Glu	Leu	Asn	Asn	Gln	Ile	Asp	Lys	Ala	Ser	Ser	Val	Ser	Pro	Thr	245	250	255	

Asp Tyr

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

09765372.012201

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

GGATGCTCAA GAAACTGCGG GAGTTCAC TA AATATGTG GCAGATTCAG AGCTATCATC      60
AGAAGAAAAG AAGCAGCTTG TCTATGATAT TCCGACATAC GTGGAGAATG ATGATGAAAC      120
TTATTATCTT GTTTATAAGT TAAATTCTCA AAATCAACTG GCGGAATTGC CAAATACTGG      180
AAGCAAGAAT GAGAGGCAA                                          199

```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Asp Ala Gln Glu Thr Ala Gly Val His Tyr Lys Tyr Val Ala Asp Ser
1           5           10           15

Glu Leu Ser Ser Glu Glu Lys Lys Gln Leu Val Tyr Asp Ile Pro Thr
          20           25           30

Tyr Val Glu Asn Asp Asp Glu Thr Tyr Tyr Leu Val Tyr Lys Leu Asn
          35           40           45

Ser Gln Asn Gln Leu Ala Glu Leu Pro Asn Thr Gly Ser Lys Asn Glu
          50           55           60

Arg Gln
65

```

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

CGACAAAGGT GAGACTGAGG TTCAACCAGA GTCGCCAGAT ACTGTGGTAA GTGATAAAGG      60
TGAACCAGAG CAGGTAGCAC CGCTTCCAGA ATATAAGGGT AATATTGAGC AAGTAAAACC      120
TGAAACTCCG GTTGAGAAGA CCAAAGAACA AGGTCCAGAA AAAACTGAAG AAGTTCCAGT      180
AAAACCAACA GAAGAAACAC CAGTAAATCC AAATGAAGGT ACTACAGAAG GAACCTCAAT      240

```

09765272-012201



TCAAGAAGCA GAAAATCCAG TTCAACCTGC AGAAGAATCA ACAACGAATT CAGAGAAAGT 300  
 ATCACCAGAT ACATCTAGCA AAAATACTGG GGAAGTGTCC AGTAATCCTA GTGATTTCGAC 360  
 AACCTCAGTT GGAGAATCAA ATAAACCAGA ACATAATGAC TCTAAAAATG AAAATTCAGA 420  
 AAAAAGTGTGTA GAAGAAGTTC CAGTAAATCC AAATGAAGGC ACAGTAGAAG GTACCTCAAA 480  
 TCAAGAAACA GAAAAACCAG TTCAACCTGC AGAAGAAACA CAAACAAACT CTGGGAAAAAT 540  
 AGCTAACGAA AATACTGGAG AAGTATCCAA TAAACCTAGT GATTCAAAAC CACCAGTTGA 600  
 AGAATCAAAT CAACCAGAAA AAAACGGAAC TGCAACAAAA CCAGAAAATT CAGGTAATAC 660  
 AACATCAGAG AATGGACAAA CAGAACCAGA ACCATCAAAC GGAAATTCAA CTGAGGATGT 720  
 TTCAACCGAA TCAAACACAT CCAATTCAAA TGGAAACGAA GAAATTAAAC AAGAAAATGA 780  
 ACTAGACCCT GATAAAAAGG TAGAAGAACC AGAGAAAACA CTTGAATTAA GAAAT 835

## (2) INFORMATION FOR SEQ ID NO:94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp	Lys	Gly	Glu	Thr	Glu	Val	Gln	Pro	Glu	Ser	Pro	Asp	Thr	Val	Val	1	5	10	15
Ser	Asp	Lys	Gly	Glu	Pro	Glu	Gln	Val	Ala	Pro	Leu	Pro	Glu	Tyr	Lys	20	25	30	
Gly	Asn	Ile	Glu	Gln	Val	Lys	Pro	Glu	Thr	Pro	Val	Glu	Lys	Thr	Lys	35	40	45	
Glu	Gln	Gly	Pro	Glu	Lys	Thr	Glu	Glu	Val	Pro	Val	Lys	Pro	Thr	Glu	50	55	60	
Glu	Thr	Pro	Val	Asn	Pro	Asn	Glu	Gly	Thr	Thr	Glu	Gly	Thr	Ser	Ile	65	70	75	80
Gln	Glu	Ala	Glu	Asn	Pro	Val	Gln	Pro	Ala	Glu	Glu	Ser	Thr	Thr	Asn	85	90	95	
Ser	Glu	Lys	Val	Ser	Pro	Asp	Thr	Ser	Ser	Lys	Asn	Thr	Gly	Glu	Val	100	105	110	
Ser	Ser	Asn	Pro	Ser	Asp	Ser	Thr	Thr	Ser	Val	Gly	Glu	Ser	Asn	Lys	115	120	125	
Pro	Glu	His	Asn	Asp	Ser	Lys	Asn	Glu	Asn	Ser	Glu	Lys	Thr	Val	Glu	130	135	140	
Glu	Val	Pro	Val	Asn	Pro	Asn	Glu	Gly	Thr	Val	Glu	Gly	Thr	Ser	Asn	145	150	155	160

09765272-012201

Gln Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn  
 165 170 175

Ser Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro  
 180 185 190

Ser Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn  
 195 200 205

Gly Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn  
 210 215 220

Gly Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val  
 225 230 235 240

Ser Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys  
 245 250 255

Gln Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys  
 260 265 270

Thr Leu Glu Leu Arg Asn  
 275

## (2) INFORMATION FOR SEQ ID NO: 95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAATCAATTG GTAGCACAAG ATCCAAAAGC ACAAGATAGC ACTAAACTGA CTGCTGAAAA	60
ATCAACTGTT AAAGCACCTG CTCAAAGAGT AGATGTAAAA GATATAACTC ATTTAACAGA	120
TGAAGAAAAA GTTAAGGTTG CTATTTTACA AGCAAATGGT TCAGCATTAG ACGGAGCGAC	180
AATCAATGTA GCTGGAGATG GTACAGCAAC AATCACATTC CCAGATGGTT CAGTAGTGAC	240
GATTCTAGGA AAAGATACAG TTCAACAATC TGCGAAAGGT GAATCTGTAA CTCAAGAAGC	300
TACACCAGAG TATAAGCTAG AAAATACACC AGGTGGAGAT AAGGGAGGCA ATACTGGAAG	360
CTCAGATGCT AATGCGAATG AAGGCGGTGG TAGCCAGGCG GGTGGATCAG CTCACACAGG	420
TTCACAAAAC TCAGCTCAAT CACAAGCTTC TAAGCAATTA GCTACTGAAA AAGAATCAGC	480
TAAAAATGCC ATTGAAAAAG CAGCCAAGGA CAAGCAGGAT GAAATCAAAG GCGCACCGCT	540
TTCTGATAAA GAAAAAGCAG AACTTTTAGC AAGAGTGGAA GCAGAAAAAC AAGCAGCTCT	600
CAAAGAGATT GAAATGCGA AACTATGGA AGATGTGAAG GAAGCAGAAA CGATTGGAGT	660
GCAAGCCATT GCCATGGTTA CAGTTCCTAA GAGACCAGTG GCTCCTAAT	709

## (2) INFORMATION FOR SEQ ID NO: 96:

## (i) SEQUENCE CHARACTERISTICS:

09765272.012201

- (A) LENGTH: 236 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Asn Gln Leu Val Ala Gln Asp Pro Lys Ala Gln Asp Ser Thr Lys Leu  
 1 5 10 15  
 Thr Ala Glu Lys Ser Thr Val Lys Ala Pro Ala Gln Arg Val Asp Val  
 20 25 30  
 Lys Asp Ile Thr His Leu Thr Asp Glu Glu Lys Val Lys Val Ala Ile  
 35 40 45  
 Leu Gln Ala Asn Gly Ser Ala Leu Asp Gly Ala Thr Ile Asn Val Ala  
 50 55 60  
 Gly Asp Gly Thr Ala Thr Ile Thr Phe Pro Asp Gly Ser Val Val Thr  
 65 70 75 80  
 Ile Leu Gly Lys Asp Thr Val Gln Gln Ser Ala Lys Gly Glu Ser Val  
 85 90 95  
 Thr Gln Glu Ala Thr Pro Glu Tyr Lys Leu Glu Asn Thr Pro Gly Gly  
 100 105 110  
 Asp Lys Gly Gly Asn Thr Gly Ser Ser Asp Ala Asn Ala Asn Glu Gly  
 115 120 125  
 Gly Gly Ser Gln Ala Gly Gly Ser Ala His Thr Gly Ser Gln Asn Ser  
 130 135 140  
 Ala Gln Ser Gln Ala Ser Lys Gln Leu Ala Thr Glu Lys Glu Ser Ala  
 145 150 155 160  
 Lys Asn Ala Ile Glu Lys Ala Ala Lys Asp Lys Gln Asp Glu Ile Lys  
 165 170 175  
 Gly Ala Pro Leu Ser Asp Lys Glu Lys Ala Glu Leu Leu Ala Arg Val  
 180 185 190  
 Glu Ala Glu Lys Gln Ala Ala Leu Lys Glu Ile Glu Asn Ala Lys Thr  
 195 200 205  
 Met Glu Asp Val Lys Glu Ala Glu Thr Ile Gly Val Gln Ala Ile Ala  
 210 215 220  
 Met Val Thr Val Pro Lys Arg Pro Val Ala Pro Asn  
 225 230 235

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

09765272.012201

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CAAACAGTCA GCTTCAGGAA CGATTGAGGT GATTTCACGA GAAAATGGCT CTGGGACACG 60  
GGGTGCCTTC ACAGAAATCA CAGGGATTCT CAAAAAGAC GGTGATAAAA AAATTGACAA 120  
CACTGCCAAA ACAGCTGTGA TTCAAATAG TACAGAAGGT GTTCTCTCAG CAGTTCAAGG 180  
GAATGCTAAT GCTATCGGCT ACATCTCCTT GGGATCTTTA ACGAAATCTG TCAAGGCTTT 240  
AGAGATTGAT GGTGTCAAGG CTAGTCGAGA CACAGTTTAA GATGGTGAAT ACCCTCTTCA 300  
ACGTCCCTTC AACATTGTTT GGTCTTCTAA TCTTTCCAAG CTAGGTCAAG ATTTTATCAG 360  
CTTTATCCAC TCCAAACAAG GTCAACAAGT GGTCACAGAT AATAAATTTA TTGAAGCTAA 420  
AACCGAAACC ACGGAATATA CAAGCCAACA CTTATCAGGC AAGTTGTCTG TTGTAGGTTT 480  
CACTTCAGTA TCTTCTTTAA TGGAAAAATT AGCAGAAGCT TATAAAAAAG AAAATCCAGA 540  
AGTTACGATT GATATTACCT CTAATGGGTC TTCAGCAGGT ATTACCGCTG TTAAGGAGAA 600  
AACCGCTGAT ATTGGTATGG TTTCTAGGGA ATTAACCTCT GAAGAAGGTA AGAGTCTCAC 660  
CCATGATGCT ATTGCTTTAG ACGGTATTGC TGTTGTGGTC AATAATGACA ATAAGGCAAG 720  
CCAAGTCAGT ATGGCTGAAC TTGCAGACGT TTTTAGTGGC AAATTAACCA CCTGGGACAA 780  
GATTAAA 787

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Lys Gln Ser Ala Ser Gly Thr Ile Glu Val Ile Ser Arg Glu Asn Gly  
1 5 10 15  
Ser Gly Thr Arg Gly Ala Phe Thr Glu Ile Thr Gly Ile Leu Lys Lys  
20 25 30  
Asp Gly Asp Lys Lys Ile Asp Asn Thr Ala Lys Thr Ala Val Ile Gln  
35 40 45  
Asn Ser Thr Glu Gly Val Leu Ser Ala Val Gln Gly Asn Ala Asn Ala  
50 55 60  
Ile Gly Tyr Ile Ser Leu Gly Ser Leu Thr Lys Ser Val Lys Ala Leu  
65 70 75 80  
Glu Ile Asp Gly Val Lys Ala Ser Arg Asp Thr Val Leu Asp Gly Glu  
85 90 95

09765272.012201

Tyr Pro Leu Gln Arg Pro Phe Asn Ile Val Trp Ser Ser Asn Leu Ser  
 100 105 110  
 Lys Leu Gly Gln Asp Phe Ile Ser Phe Ile His Ser Lys Gln Gly Gln  
 115 120 125  
 Gln Val Val Thr Asp Asn Lys Phe Ile Glu Ala Lys Thr Glu Thr Thr  
 130 135 140  
 Glu Tyr Thr Ser Gln His Leu Ser Gly Lys Leu Ser Val Val Gly Ser  
 145 150 155 160  
 Thr Ser Val Ser Ser Leu Met Glu Lys Leu Ala Glu Ala Tyr Lys Lys  
 165 170 175  
 Glu Asn Pro Glu Val Thr Ile Asp Ile Thr Ser Asn Gly Ser Ser Ala  
 180 185 190  
 Gly Ile Thr Ala Val Lys Glu Lys Thr Ala Asp Ile Gly Met Val Ser  
 195 200 205  
 Arg Glu Leu Thr Pro Glu Glu Gly Lys Ser Leu Thr His Asp Ala Ile  
 210 215 220  
 Ala Leu Asp Gly Ile Ala Val Val Val Asn Asn Asp Asn Lys Ala Ser  
 225 230 235 240  
 Gln Val Ser Met Ala Glu Leu Ala Asp Val Phe Ser Gly Lys Leu Thr  
 245 250 255  
 Thr Trp Asp Lys Ile Lys  
 260

## (2) INFORMATION FOR SEQ ID NO: 99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATTCGATGAT GCGGATGAAA AGATGACCCG TGATGAAATT GCCTATATGC TGACAAATAG 60  
 TGAAGAAACA TTGGATGCTG ATGAGATTGA GATGCTACAA GGTGTCTTTT CGCTCGATGA 120  
 ACTGATGGCA CGAGAGGTTA TGGTTCCTCG AACGGATGCC TTTATGGTGG ATATTCAGGA 180  
 TGATAGTCAA GCCATTATCC AAAGTATTTT AAAACAAAAT TATTCTCGTA TCCCGGTTTA 240  
 TGATGGGGAT AAGGACAATG TAATTGGAAT CATTACACC AAGAGTCTCC TTAAGGCAGG 300  
 CTTTGTGGAC GGTTTTGACA ATATTGTTTG GAAGAGAATT TTACAAGATC CACTTTTTGT 360  
 ACCTGAAACT ATTTTTGTGG ATGACTTGCT AAAAGAACTG CGAAATACCC AAAGACAAAT 420  
 G 421

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Phe Asp Asp Ala Asp Glu Lys Met Thr Arg Asp Glu Ile Ala Tyr Met
1          5          10          15
Leu Thr Asn Ser Glu Glu Thr Leu Asp Ala Asp Glu Ile Glu Met Leu
20        25        30
Gln Gly Val Phe Ser Leu Asp Glu Leu Met Ala Arg Glu Val Met Val
35        40        45
Pro Arg Thr Asp Ala Phe Met Val Asp Ile Gln Asp Asp Ser Gln Ala
50        55        60
Ile Ile Gln Ser Ile Leu Lys Gln Asn Tyr Ser Arg Ile Pro Val Tyr
65        70        75        80
Asp Gly Asp Lys Asp Asn Val Ile Gly Ile Ile His Thr Lys Ser Leu
85        90        95
Leu Lys Ala Gly Phe Val Asp Gly Phe Asp Asn Ile Val Trp Lys Arg
100       105       110
Ile Leu Gln Asp Pro Leu Phe Val Pro Glu Thr Ile Phe Val Asp Asp
115       120       125
Leu Leu Lys Glu Leu Arg Asn Thr Gln Arg Gln Met
130       135       140

```

## (2) INFORMATION FOR SEQ ID NO: 101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

GGAGAGTCGA TCAAAAGTAG ATGAAGCTGT GTCTAAGTTT GAAAAGGACT CATCTTCTTC      60
GTCAAGTTCA GACTCTTCCA CTAAACCGGA AGCTTCAGAT ACAGCGAAGC CAAACAAGCC      120
GACAGAACCA GGAGAAAAGG TAGCAGAAGC TAAGAAGAAG GTTGAAGAAG CTGAGAAAAA      180
AGCCAAGGAT CAAAAGAAG AAGATCGTCG TAACTACCCA ACCATTACTT ACAAACGCT      240
TGAAGTTGAA ATTGCTGAGT CCGATGTGGA AGTTAAAAAA GCGGAGCTTG AACTAGTAAA      300
AGTGAAAGCT AACGAACCTC GAGACGAGCA A                                331

```

## (2) INFORMATION FOR SEQ ID NO:102:

09765272.012204

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 110 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Glu Ser Arg Ser Lys Val Asp Glu Ala Val Ser Lys Phe Glu Lys Asp
1      5      10      15
Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr Lys Pro Glu Ala Ser
20     25     30
Asp Thr Ala Lys Pro Asn Lys Pro Thr Glu Pro Gly Glu Lys Val Ala
35     40     45
Glu Ala Lys Lys Lys Val Glu Glu Ala Glu Lys Lys Ala Lys Asp Gln
50     55     60
Lys Glu Glu Asp Arg Arg Asn Tyr Pro Thr Ile Thr Tyr Lys Thr Leu
65     70     75     80
Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu
85     90     95
Glu Leu Val Lys Val Lys Ala Asn Glu Pro Arg Asp Glu Gln
100    105    110

```

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 358 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

ATGGACAACA GGAAACTGGG ACGAGGTTAT ATCTGGTAAG ATTGACAAGT ACAAAGATCC      60
AGATATTCCA ACAGTTGAAT CACAAGAAGT TACGTCAGAC TCTAGTGATA AAGAAATAAC      120
GGTAAGGTAT GACCGTTTAT CAACACCAGA AAAACCAATC CCACAACCAA ATCCAGAGCA      180
TCCAAGTGTT CCGACACCAA ACCCAGAACT ACCAAATCAA GAGACTCCAA CACCAGATAA      240
ACCAACTCCA GAACCAGGTA CTCCAAAAAC TGAAACTCCA GTGAATCCAG ACCCAGAAGT      300
TCCGACTTAT GAGACAGGTA AGAGAGAGGA ATTGCCAAAC ACAGGTACAG AAGCTAAT      358

```

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

09765272.012201

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

Trp Thr Thr Gly Asn Trp Asp Glu Val Ile Ser Gly Lys Ile Asp Lys
1           5           10           15
Tyr Lys Asp Pro Asp Ile Pro Thr Val Glu Ser Gln Glu Val Thr Ser
20          25          30
Asp Ser Ser Asp Lys Glu Ile Thr Val Arg Tyr Asp Arg Leu Ser Thr
35          40          45
Pro Glu Lys Pro Ile Pro Gln Pro Asn Pro Glu His Pro Ser Val Pro
50          55          60
Thr Pro Asn Pro Glu Leu Pro Asn Gln Glu Thr Pro Thr Pro Asp Lys
65          70          75          80
Pro Thr Pro Glu Pro Gly Thr Pro Lys Thr Glu Thr Pro Val Asn Pro
85          90          95
Asp Pro Glu Val Pro Thr Tyr Glu Thr Gly Lys Arg Glu Glu Leu Pro
100         105         110
Asn Thr Gly Thr Glu Ala Asn
115

```

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

CGATGGGCTC AATCCAACCC CAGGTCAAGT CTTACCTGAA GAGACATCGG GAACGAAAGA      60
GGGTGACTTA TCAGAAAAAC CAGGAGACAC CGTTCTCACT CAAGCGAAAC CTGAGGGCGT      120
TACTGGAAAT ACGAATTCAC TTCCGACACC TACAGAAAGA ACTGAAGTGA GCGAGGAAAC      180
AAGCCCTTCT AGTCTGGATA CACTTTTTGA AAAAGATGAA GAAGCTCAAA AAAATCCAGA      240
GCTAACAGAT GTCTTAAAG AAACTGTAGA TACAGCTGAT GTGGATGGGA CACAAGCAAG      300
TCCAGCAGAA ACTACTCCTG AACAAGTAAA AGGTGGAGTG AAAGAAAATA CAAAAGACAG      360
CATCGATGTT CCTGCTGCTT ATCTTGAAAA AGCTGAAGGG AAAGGTCCTT TCACTGCCGG      420
TGTAACCAA GTAATTCCTT ATGAATATT CGCTGGTGAT GGTATGTAA CTCGTCTATT      480
ACTAAAAGCT TCGGATAATG CTCCTTGGTC TGACAATGGT ACTGCTAAAA ATCCTGCTTT      540
ACCTCCTCTT GAAGGATTAA CAAAAGGGAA ATACTTCTAT GAAGTAGACT TAAATGGCAA      600

```



TACTGTTGGT AAACAAGGTC AAGCTTTAAT TGATCAACTT CGCGCTAATG GTACTCAAAC 660  
 TTATAAAGCT ACTGTTAAAG TTTACGGAAA TAAAGACGGT AAAGCTGACT TGACTAATCT 720  
 AGTTGCTACT AAAAATGTAG ACATCAACAT CAATGGATTA GTTGCTAAAG AAACAGTTCA 780  
 AAAAGCCGTT GCAGACAACG TTAAAGACAG TATCGATGTT CCAGCAGCCT ACCTAGAAAA 840  
 AGCCAAGGGT GAAGGTCCAT TCACAGCAGG TGTCAACCAT GTGATTCCAT ACGAACTCTT 900  
 CGCAGGTGAT GGCATGTTGA CTCGTCTCTT GCTCAAGGCA TCTGACAAGG CACCATGGTC 960  
 AGATAACGGC GACGCTAAAA ACCCAGCCCT ATCTCCACTA GCGGAAAACG TGAAGACCAA 1020  
 AGGTCAATAC TTCTATCAAN TAGCCTTGGA CGGAAATGTA GCTGGCAAAG AAAACAAGC 1080  
 GCTCATTGAC CAGTTCCGAG CAAANGGTAC TCAAACCTAC AGCGCTACAG TCAATGTCTA 1140  
 TGGTAACAAA GACGGTAAAC CAGACTTGGA CAACATCGTA GCAACTAAAA AAGTCACTAT 1200  
 TAACATAAAC GGTTTAATTT CTAAAGAAAC AGTTCAAAAA GCCGTTGCAG ACAACGTTAA 1260  
 NGACAGTATC GATGTTCCAG CAGCCTACCT AGAAAAAGCC AAGGGTGAAG GTCCATTAC 1320  
 AGCAGGTGTC AACCATGTGA TTCCATACGA ACTCTTCGCA GGTGATGGTA TGTTGACTCG 1380  
 TCTCTTGCTC AAGGCATCTG ACAAGGCACC ATGGTCAGAT AACGGNGACG CTAAAAACCC 1440  
 AGCNCTATCT CCACTAGGTG AAAACGTGAA GACCAAAGGT CAATACTTCT ATCAANTAGC 1500  
 CTTGGACGGA AATGTAGCTG GCAAAGAAAA ACAAGCGCTC ATTGACCAGT TCCGAGCAAA 1560  
 CGGTACTCAA ACTTACAGCG CTACAGTCAA TGTCTATGGT AACAAAGACG GTAAACCAGA 1620  
 CTTGGACAAC ATCGTAGCAA CTAAAAAGT CACTATTAAG ATAAATGTTA AAGAAACATC 1680  
 AGACACAGCA AATGGTTCAT TATCACCTTC TAACTCTGGT TCTGGCGTGA CTCCGATGAA 1740  
 TCACAATCAT GCTACAGGTA CTACAGATAG CATGCCTGCT GACACCATGA CAAGTTCTAC 1800  
 CAACACGATG GCAGGTGAAA ACATGGCTGC TTCTGCTAAC AAGATGTCTG ATACGATGAT 1860  
 GTCAGAGGAT AAAGCTATG 1879

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Asp Gly Leu Asn Pro Thr Pro Gly Gln Val Leu Pro Glu Glu Thr Ser  
 1 5 10 15  
 Gly Thr Lys Glu Gly Asp Leu Ser Glu Lys Pro Gly Asp Thr Val Leu  
 20 25 30

Thr	Gln	Ala	Lys	Pro	Glu	Gly	Val	Thr	Gly	Asn	Thr	Asn	Ser	Leu	Pro		
		35					40					45					
Thr	Pro	Thr	Glu	Arg	Thr	Glu	Val	Ser	Glu	Glu	Thr	Ser	Pro	Ser	Ser		
	50					55					60						
Leu	Asp	Thr	Leu	Phe	Glu	Lys	Asp	Glu	Glu	Ala	Gln	Lys	Asn	Pro	Glu		
65					70					75					80		
Leu	Thr	Asp	Val	Leu	Lys	Glu	Thr	Val	Asp	Thr	Ala	Asp	Val	Asp	Gly		
				85					90					95			
Thr	Gln	Ala	Ser	Pro	Ala	Glu	Thr	Thr	Pro	Glu	Gln	Val	Lys	Gly	Gly		
			100					105						110			
Val	Lys	Glu	Asn	Thr	Lys	Asp	Ser	Ile	Asp	Val	Pro	Ala	Ala	Tyr	Leu		
		115					120					125					
Glu	Lys	Ala	Glu	Gly	Lys	Gly	Pro	Phe	Thr	Ala	Gly	Val	Asn	Gln	Val		
	130					135						140					
Ile	Pro	Tyr	Glu	Leu	Phe	Ala	Gly	Asp	Gly	Met	Leu	Thr	Arg	Leu	Leu		
145					150					155					160		
Leu	Lys	Ala	Ser	Asp	Asn	Ala	Pro	Trp	Ser	Asp	Asn	Gly	Thr	Ala	Lys		
				165					170						175		
Asn	Pro	Ala	Leu	Pro	Pro	Leu	Glu	Gly	Leu	Thr	Lys	Gly	Lys	Tyr	Phe		
			180					185						190			
Tyr	Glu	Val	Asp	Leu	Asn	Gly	Asn	Thr	Val	Gly	Lys	Gln	Gly	Gln	Ala		
		195					200					205					
Leu	Ile	Asp	Gln	Leu	Arg	Ala	Asn	Gly	Thr	Gln	Thr	Tyr	Lys	Ala	Thr		
	210					215					220						
Val	Lys	Val	Tyr	Gly	Asn	Lys	Asp	Gly	Lys	Ala	Asp	Leu	Thr	Asn	Leu		
225					230					235					240		
Val	Ala	Thr	Lys	Asn	Val	Asp	Ile	Asn	Ile	Asn	Gly	Leu	Val	Ala	Lys		
				245				250						255			
Glu	Thr	Val	Gln	Lys	Ala	Val	Ala	Asp	Asn	Val	Lys	Asp	Ser	Ile	Asp		
		260						265					270				
Val	Pro	Ala	Ala	Tyr	Leu	Glu	Lys	Ala	Lys	Gly	Glu	Gly	Pro	Phe	Thr		
		275					280					285					
Ala	Gly	Val	Asn	His	Val	Ile	Pro	Tyr	Glu	Leu	Phe	Ala	Gly	Asp	Gly		
	290					295					300						
Met	Leu	Thr	Arg	Leu	Leu	Leu	Lys	Ala	Ser	Asp	Lys	Ala	Pro	Trp	Ser		
305					310					315					320		
Asp	Asn	Gly	Asp	Ala	Lys	Asn	Pro	Ala	Leu	Ser	Pro	Leu	Gly	Glu	Asn		
				325					330					335			
Val	Lys	Thr	Lys	Gly	Gln	Tyr	Phe	Tyr	Gln	Xaa	Ala	Leu	Asp	Gly	Asn		
			340					345					350				
Val	Ala	Gly	Lys	Glu	Lys	Gln	Ala	Leu	Ile	Asp	Gln	Phe	Arg	Ala	Xaa		
		355					360					365					

09765672-012201

Gly Thr Gln Thr Tyr Ser Ala Thr Val Asn Val Tyr Gly Asn Lys Asp  
 370 375 380  
 Gly Lys Pro Asp Leu Asp Asn Ile Val Ala Thr Lys Lys Val Thr Ile  
 385 390 395 400  
 Asn Ile Asn Gly Leu Ile Ser Lys Glu Thr Val Gln Lys Ala Val Ala  
 405 410 415  
 Asp Asn Val Xaa Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu Glu Lys  
 420 425 430  
 Ala Lys Gly Glu Gly Pro Phe Thr Ala Gly Val Asn His Val Ile Pro  
 435 440 445  
 Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu Leu Lys  
 450 455 460  
 Ala Ser Asp Lys Ala Pro Trp Ser Asp Asn Gly Asp Ala Lys Asn Pro  
 465 470 475 480  
 Ala Leu Ser Pro Leu Gly Glu Asn Val Lys Thr Lys Gly Gln Tyr Phe  
 485 490 495  
 Tyr Gln Xaa Ala Leu Asp Gly Asn Val Ala Gly Lys Glu Lys Gln Ala  
 500 505 510  
 Leu Ile Asp Gln Phe Arg Ala Asn Gly Thr Gln Thr Tyr Ser Ala Thr  
 515 520 525  
 Val Asn Val Tyr Gly Asn Lys Asp Gly Lys Pro Asp Leu Asp Asn Ile  
 530 535 540  
 Val Ala Thr Lys Lys Val Thr Ile Lys Ile Asn Val Lys Glu Thr Ser  
 545 550 555 560  
 Asp Thr Ala Asn Gly Ser Leu Ser Pro Ser Asn Ser Gly Ser Gly Val  
 565 570 575  
 Thr Pro Met Asn His Asn His Ala Thr Gly Thr Thr Asp Ser Met Pro  
 580 585 590  
 Ala Asp Thr Met Thr Ser Ser Thr Asn Thr Met Ala Gly Glu Asn Met  
 595 600 605  
 Ala Ala Ser Ala Asn Lys Met Ser Asp Thr Met Met Ser Glu Asp Lys  
 610 615 620  
 Ala Met  
 625

## (2) INFORMATION FOR SEQ ID NO: 107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

TTCCAATCAA AACAGGCAG ATGGTAACT CAATATCGTG ACAACCTTTT ACCCTGTCTA 60  
 TGA~~r~~TTTACC AAGCAAGTCG CAGGAGATAC GGCTAATGTA GAACTCCTAA TCGGTGCTGG 120  
 GACAGAACCT CATGAATACG AACCATCTGC CAAGGCAGTT GCCAAAATCC AAGATGCAGA 180  
 TACCTTCGTT TATGAAAATG AAAACATGGA AACATGGGTA CCTAAATTGC TAGATACCTT 240  
 GGATAAGAAA AAAGTAAAA CCATCAAGGC GACAGGCGAT ATGTTGCTCT TGCCAGGTGG 300  
 CGAGGAAGAA GAGGGAGACC ATGACCATGG AGAAGAAGGT CATCACCATG AGTTTGACCC 360  
 CCATGTTTGG TTATCACCAG TTCGTGCCAT tAAACTAGTA GAGCACCATC CGCGACACTT 420  
 GTCAGCAGAT TATCCTGATA AAAAAGAGAC CTTTGAGAAG AATGCAGCTG CCTATATCGA 480  
 AAAATTGCAA GCCTTGATA AGGCTTACGC AGAAGGTTTG TCTCAAGCAA AACAAAAGAG 540  
 CTTTGTGACT CAACACGCag CCTTTAACTa TCTTGCCTTG GACTATGGGA CTC 593

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Ser	Asn	Gln	Lys	Gln	Ala	Asp	Gly	Lys	Leu	Asn	Ile	Val	Thr	Thr	Phe	1	5	10	15
Tyr	Pro	Val	Tyr	Glu	Phe	Thr	Lys	Gln	Val	Ala	Gly	Asp	Thr	Ala	Asn	20	25	30	
Val	Glu	Leu	Leu	Ile	Gly	Ala	Gly	Thr	Glu	Pro	His	Glu	Tyr	Glu	Pro	35	40	45	
Ser	Ala	Lys	Ala	Val	Ala	Lys	Ile	Gln	Asp	Ala	Asp	Thr	Phe	Val	Tyr	50	55	60	
Glu	Asn	Glu	Asn	Met	Glu	Thr	Trp	Val	Pro	Lys	Leu	Leu	Asp	Thr	Leu	65	70	75	80
Asp	Lys	Lys	Lys	Val	Lys	Thr	Ile	Lys	Ala	Thr	Gly	Asp	Met	Leu	Leu	85	90	95	
Leu	Pro	Gly	Gly	Glu	Glu	Glu	Glu	Gly	Asp	His	Asp	His	Gly	Glu	Glu	100	105	110	
Gly	His	His	His	Glu	Phe	Asp	Pro	His	Val	Trp	Leu	Ser	Pro	Val	Arg	115	120	125	
Ala	Ile	Lys	Leu	Val	Glu	His	His	Pro	Arg	His	Leu	Ser	Ala	Asp	Tyr	130	135	140	
Pro	Asp	Lys	Lys	Glu	Thr	Phe	Glu	Lys	Asn	Ala	Ala	Tyr	Ile	Glu	145	150	155	160	

09765272.012201

Lys Leu Gln Ala Leu Asp Lys Ala Tyr Ala Glu Gly Leu Ser Gln Ala  
 165 170 175

Lys Gln Lys Ser Phe Val Thr Gln His Ala Ala Phe Asn Tyr Leu Ala  
 180 185 190

Leu Asp Tyr Gly Thr  
 195

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

TATCACAGGA TCGAACGGTA AGACAACCAC AACGACTATG ATTGGGGAAG TTTTGACTGC	60
TGCTGGCCAA CATGGTCTTT TATCAGGGAA TATCGGCTAT CCAGCTAGTC AGGTTGCTCA	120
AATAGCATCA GATAAGGACA CGCTTGTTAT GGAACCTTCT TCTTTCCAAC TCATGGGTGT	180
TCAAGAATTC CATCCAGAGA TTGCGGTTAT TACCAACCTC ATGCCAACTC ATATCGACTA	240
CCATGGGTCA TTTTCGGAAT ATGTAGCAGC CAAGTGAAT ATCCAGAACA AGATGACAGC	300
AGCTGATTTC CTTGTCTTGA ACTTTAATCA AGACTTGGCA AAAGACTTGA CTTCCAAGAC	360
AGAAGCCACT GTTGTACCAT TTTCAACACT TGAAAAGGTT GATGGAGCTT ATCTGGAAGA	420
TGGTCAACTC TACTTCCGTG GTGAAGTAGT CATGGCAGCG AATGAAATCG GTGTTCCAGG	480
TAGCCACAAT GTGGAAAATG CCCTTGCGAC TATTGCTGTA GCCAAGCTTC GTGATGTGGA	540
CAATCAAACC ATCAAGGAAA CTCTTTTCAGC CTTGCGGTGGT GTCAAACACC GTCTCCAGTT	600
TGTGGATGAC ATCAAGGGTG TTAAATTCTA TAACGACAGT AAATCAACTA ATATCTTGGC	660
TACTCAAAAA GCCTTGTCAG GATTTGACAA CAGCAAGGTC GTCTTGATTG CAGGTGGTTT	720
GGACCGTGGC AATGAGTTTG ACGAATTGGT GCCAGACATT ACTGGACTCA AGAAGATGGT	780
CATCCTGGGT CAATCTGCAG AACGTGTCAA ACGGGCAGCA GACAAGGCTG GTGTCGCTTA	840
TGTGGAGGCG ACAGATATTG CAGATGCGAC CCGCAAGGCC TATGAGCTTG CGACTCAAGG	900
AGATGTGGTT CTTCTTAGTC CTGCCAATGC TAGCTGGGAT ATGTATGCTA ACTTTGAAGT	960
ACGTGGCGAC CTCTTTATCG ACACAGTAGC GGAGTTAAAA GAA	1003

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

09765272.012201

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110: —

Gly Ile Thr Gly Ser Asn Gly Lys Thr Thr Thr Thr Thr Met Ile Gly  
 1 5 10 15  
 Glu Val Leu Thr Ala Ala Gly Gln His Gly Leu Leu Ser Gly Asn Ile  
 20 25 30  
 Gly Tyr Pro Ala Ser Gln Val Ala Gln Ile Ala Ser Asp Lys Asp Thr  
 35 40 45  
 Leu Val Met Glu Leu Ser Ser Phe Gln Leu Met Gly Val Gln Glu Phe  
 50 55 60  
 His Pro Glu Ile Ala Val Ile Thr Asn Leu Met Pro Thr His Ile Asp  
 65 70 75 80  
 Tyr His Gly Ser Phe Ser Glu Tyr Val Ala Ala Lys Trp Asn Ile Gln  
 85 90 95  
 Asn Lys Met Thr Ala Ala Asp Phe Leu Val Leu Asn Phe Asn Gln Asp  
 100 105 110  
 Leu Ala Lys Asp Leu Thr Ser Lys Thr Glu Ala Thr Val Val Pro Phe  
 115 120 125  
 Ser Thr Leu Glu Lys Val Asp Gly Ala Tyr Leu Glu Asp Gly Gln Leu  
 130 135 140  
 Tyr Phe Arg Gly Glu Val Val Met Ala Ala Asn Glu Ile Gly Val Pro  
 145 150 155 160  
 Gly Ser His Asn Val Glu Asn Ala Leu Ala Thr Ile Ala Val Ala Lys  
 165 170 175  
 Leu Arg Asp Val Asp Asn Gln Thr Ile Lys Glu Thr Leu Ser Ala Phe  
 180 185 190  
 Gly Gly Val Lys His Arg Leu Gln Phe Val Asp Asp Ile Lys Gly Val  
 195 200 205  
 Lys Phe Tyr Asn Asp Ser Lys Ser Thr Asn Ile Leu Ala Thr Gln Lys  
 210 215 220  
 Ala Leu Ser Gly Phe Asp Asn Ser Lys Val Val Leu Ile Ala Gly Gly  
 225 230 235 240  
 Leu Asp Arg Gly Asn Glu Phe Asp Glu Leu Val Pro Asp Ile Thr Gly  
 245 250 255  
 Leu Lys Lys Met Val Ile Leu Gly Gln Ser Ala Glu Arg Val Lys Arg  
 260 265 270  
 Ala Ala Asp Lys Ala Gly Val Ala Tyr Val Glu Ala Thr Asp Ile Ala  
 275 280 285  
 Asp Ala Thr Arg Lys Ala Tyr Glu Leu Ala Thr Gln Gly Asp Val Val  
 290 295 300  
 Leu Leu Ser Pro Ala Asn Ala Ser Trp Asp Met Tyr Ala Asn Phe Glu

09765272.012201

305

310

315

320

Val Arg Gly Asp Leu Phe Ile Asp Thr Val Ala Glu Leu Lys Glu  
 325 330 335

## (2) INFORMATION FOR SEQ ID NO: 111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AAGTTCATCG AAGATGGTTG GGAAGTCCAC TATATCGGGG ACAAGTGTGG TATCGAACAC 60  
 CAAGAAATCC TTAAGTCAGG TTTGGATGTC ACCTTCCATT CTATTGCGAC TGGAAAATTG 120  
 CGTCGCTATT TCTCTGGCA AAATATGCTG GACGTCTTCA AAGTTGGTTG GGAATTGTC 180  
 CAATCGCTCT TTATCATGTT GCGACTGCGT CCACAGACCE TTTTTCAAA GGGGGGCTTT 240  
 GTCTCAGTAC CGCCTGTTAT CGCTGCGCGT GTGTCAGGAG TGCCTGTCTT TATTCACGAA 300  
 TCTGACCTGT CTATGGGCTT GGCCAATAAA ATCGCCTATA AATTTGCGAC TAAGATGTAT 360  
 TCAACCTTTG AACAAAGCTTC GAGTTTGGCT AAGGTTGAGC ATGTGGGAGC GG 412

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ser Ser Ser Lys Met Val Gly Lys Ser Thr Ile Ser Gly Thr Ser Val  
 1 5 10 15  
 Val Ser Asn Thr Lys Lys Ser Leu Ser Gln Val Trp Met Ser Pro Ser  
 20 25 30  
 Ile Leu Leu Arg Leu Glu Asn Cys Val Ala Ile Ser Leu Gly Lys Ile  
 35 40 45  
 Cys Trp Thr Ser Ser Lys Leu Val Gly Glu Leu Ser Asn Arg Ser Leu  
 50 55 60  
 Ser Cys Cys Asp Cys Val His Arg Pro Phe Phe Gln Arg Gly Ala Leu  
 65 70 75 80  
 Ser Gln Tyr Arg Leu Leu Ser Leu Arg Val Cys Gln Glu Cys Leu Ser  
 85 90 95  
 Leu Phe Thr Asn Leu Thr Cys Leu Trp Ala Trp Pro Ile Lys Ser Pro

09765272-012204

225

100

105

110

Ile Asn Leu Arg Leu Arg Cys Ile Gln Pro Leu Asn Lys Leu Arg Val  
115 120 125

Trp Leu Arg Leu Ser Met Trp Glu Arg  
130 135

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

ATCGCTAGCT AGTGAAATGC AAGAAAGTAC ACGTAAATTC AAGGTTACTG CTGACCTAAC	60
AGATGCCGGT GTTGAACGA TTGAAGTTCC TTTGAGCATT GAAGATTTAC CCAATGGGCT	120
GACCGCTGTG GCGACTCCGC AAAAAATTAC AGTCAAGATT GGTAAGAAGG CTCAGAAGGA	180
TAAGGTAAAG ATTGTACCAG AGATTGACCC TAGTCAAATT GATAGTCGGG TACAAATTGA	240
AAATGTCATG GTGTCAGATA AAGAAGTGTC TATTACGAGT GACCAAGAGA CATTGGATAG	300
AATTGATAAG ATTATCGCTG TTTTGCCAAC TAGCGAACGT ATAACAGGTA ATTACAGTGG	360
TTCAGTACCT TTGCAGGCAA TCGACCGCAA TGGTGTGTGTC TTACCGGCAG TTATCACTCC	420
GTTTGATACA ATAATGAAGG TGACTIONAAA ACCAGTAGCA CCAAGTTCAA GCACATCAAA	480
TTCAAGTACA AGCAGTTCAT CGGAGACATC TTCGTCAACG AAAGCAACTA GTTCAAAAAC	540
GAAT	544

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ser Leu Ala Ser Glu Met Gln Glu Ser Thr Arg Lys Phe Lys Val Thr  
1 5 10 15

Ala Asp Leu Thr Asp Ala Gly Val Gly Thr Ile Glu Val Pro Leu Ser  
20 25 30

Ile Glu Asp Leu Pro Asn Gly Leu Thr Ala Val Ala Thr Pro Gln Lys  
35 40 45

Ile Thr Val Lys Ile Gly Lys Lys Ala Gln Lys Asp Lys Val Lys Ile

09765272.012201



50	55	60
Val Pro Glu Ile Asp	Pro Ser Gln Ile Asp	Ser Arg Val Gln Ile Glu
65	70	75 80
Asn Val Met Val Ser Asp	Lys Glu Val Ser Ile Thr Ser Asp	Gln Glu
85	90	95
Thr Leu Asp Arg Ile Asp	Lys Ile Ile Ala Val Leu Pro Thr Ser Glu	
100	105	110
Arg Ile Thr Gly Asn Tyr Ser Gly Ser Val Pro Leu Gln Ala Ile Asp		
115	120	125
Arg Asn Gly Val Val Leu Pro Ala Val Ile Thr Pro Phe Asp Thr Ile		
130	135	140
Met Lys Val Thr Thr Lys Pro Val Ala Pro Ser Ser Ser Thr Ser Asn		
145	150	155 160
Ser Ser Thr Ser Ser Ser Ser Glu Thr Ser Ser Ser Thr Lys Ala Thr		
165	170	175
Ser Ser Lys Thr Asn		
180		

## (2) INFORMATION FOR SEQ ID NO: 115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GCACCAGATG GGGCACAAGG TTCAGGGATC AGATGTTGAA AAGTACTACT TTACCCAACG	60
CGGTCTTGAG CAGGCAGGAA TTACCATTCT TCCTTTTGAT GAAAAAATC TAGACGGTGA	120
TATGGAAATT ATCGCTGGAA ATGCCTTTTCG TCCAGATAAC AACGTCGAAA TTGCCTATGC	180
GGACCAAAT GGTATCAGCT ACAAACGTTA CCATGAGTTT CTAGGTAGCT TTATGCGTGA	240
CTTTGTTAGC ATGGGAGTAG CAGGAGCACA TGGAAAACT TCAACGACAG GTATGTTGTC	300
TCATGTCTTG TCTCACATTA CAGATACCAG CTTCTTGATT GGAGATGGGA CAGGTCGTGG	360
TTCGGCCAAT GCCAAATATT TTGTCTTTGA ATCTGACGAA TATGAGCGTC ACTTCATGCC	420
TTACCACCCA GAATACTCTA TTATCACCAA CATTGACTTT GACCATCCAG ATTATTTTAC	480
AAGTCTCGAG GATGTTTTTA ATGCCTTTAA CGACTATGCC AAACAAATCA CCAAGGGTCT	540
TTTTGTCTAT GGTGAAGATG CTGAATTGCG TAAGATTACG TCTGATGCAC CAATTTATTA	600
TTATGGTTTT GAAGCTGAAG GCAATGACTT TGTAGCTAGT GATCTTCTTC GTTCAATAAC	660
TGGTTCAACC TTCACCGTTC ATTTCCGTGG ACAAACCTTG GGGCAATTCC ACATTCCAAC	720
CTTTGGTCGT CACAATATCA TGAATGCGAC AGCCGTTATT GGTCTTCTTT ACACAGCAGG	780

09765272.012201

ATTTGATTTG AACTTGGTGC GTGAGCACTT GAAAACATTT GCCGGTGTTA AACGTCGTTT 840  
 CACTGAGAAA ATTGTCAATG ATACAGTGAT TATCGATGAC TTTGCCCCACC ATCCAACAGA 900  
 AATTATTGCG ACCTTGGATG CGGCTCGTCA GAAATACCCA AGCAAGGAAA TTGTAGCAGT 960  
 CTTTCAACCG CATACTTTA CAAGAACCAT TGCCTTGTTG GACGACTTTG CCCATGCTTT 1020  
 AAACCAAGCA GATGCTGTTT ATCTAGCGCA AATTTATGGC TCGGCTCGTG AAGTAGATCA 1080  
 TGGTGACGTT AAGGTAGAAG ACCTAGCCAA CAAAATCAAC AAAAAACACC AAGTGATTAC 1140  
 TGTGAAAAT GTTTCTCCAC TCCTAGACCA TGACAATGCT GTTTACGTCT TTATGGGAGC 1200  
 AGGAGACATC CAAACCTATG AATACTCATT TGAGCGTCTC TTGTCTAACT TGACAAGCAA 1260  
 TGTTCAA 1267

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

His	Gln	Met	Gly	His	Lys	Val	Gln	Gly	Ser	Asp	Val	Glu	Lys	Tyr	Tyr	1	5	10	15
Phe	Thr	Gln	Arg	Gly	Leu	Glu	Gln	Ala	Gly	Ile	Thr	Ile	Leu	Pro	Phe	20	25	30	
Asp	Glu	Lys	Asn	Leu	Asp	Gly	Asp	Met	Glu	Ile	Ile	Ala	Gly	Asn	Ala	35	40	45	
Phe	Arg	Pro	Asp	Asn	Asn	Val	Glu	Ile	Ala	Tyr	Ala	Asp	Gln	Asn	Gly	50	55	60	
Ile	Ser	Tyr	Lys	Arg	Tyr	His	Glu	Phe	Leu	Gly	Ser	Phe	Met	Arg	Asp	65	70	75	80
Phe	Val	Ser	Met	Gly	Val	Ala	Gly	Ala	His	Gly	Lys	Thr	Ser	Thr	Thr	85	90	95	
Gly	Met	Leu	Ser	His	Val	Leu	Ser	His	Ile	Thr	Asp	Thr	Ser	Phe	Leu	100	105	110	
Ile	Gly	Asp	Gly	Thr	Gly	Arg	Gly	Ser	Ala	Asn	Ala	Lys	Tyr	Phe	Val	115	120	125	
Phe	Glu	Ser	Asp	Glu	Tyr	Glu	Arg	His	Phe	Met	Pro	Tyr	His	Pro	Glu	130	135	140	
Tyr	Ser	Ile	Ile	Thr	Asn	Ile	Asp	Phe	Asp	His	Pro	Asp	Tyr	Phe	Thr	145	150	155	160
Ser	Leu	Glu	Asp	Val	Phe	Asn	Ala	Phe	Asn	Asp	Tyr	Ala	Lys	Gln	Ile				

09765272.012201

228

165

170

175

Thr Lys Gly Leu Phe Val Tyr Gly Glu Asp Ala Glu Leu Arg Lys Ile  
 180 185 190  
 Thr Ser Asp Ala Pro Ile Tyr Tyr Tyr Gly Phe Glu Ala Glu Gly Asn  
 195 200 205  
 Asp Phe Val Ala Ser Asp Leu Leu Arg Ser Ile Thr Gly Ser Thr Phe  
 210 215 220  
 Thr Val His Phe Arg Gly Gln Asn Leu Gly Gln Phe His Ile Pro Thr  
 225 230 235 240  
 Phe Gly Arg His Asn Ile Met Asn Ala Thr Ala Val Ile Gly Leu Leu  
 245 250 255  
 Tyr Thr Ala Gly Phe Asp Leu Asn Leu Val Arg Glu His Leu Lys Thr  
 260 265 270  
 Phe Ala Gly Val Lys Arg Arg Phe Thr Glu Lys Ile Val Asn Asp Thr  
 275 280 285  
 Val Ile Ile Asp Asp Phe Ala His His Pro Thr Glu Ile Ile Ala Thr  
 290 295 300  
 Leu Asp Ala Ala Arg Gln Lys Tyr Pro Ser Lys Glu Ile Val Ala Val  
 305 310 315 320  
 Phe Gln Pro His Thr Phe Thr Arg Thr Ile Ala Leu Leu Asp Asp Phe  
 325 330 335  
 Ala His Ala Leu Asn Gln Ala Asp Ala Val Tyr Leu Ala Gln Ile Tyr  
 340 345 350  
 Gly Ser Ala Arg Glu Val Asp His Gly Asp Val Lys Val Glu Asp Leu  
 355 360 365  
 Ala Asn Lys Ile Asn Lys Lys His Gln Val Ile Thr Val Glu Asn Val  
 370 375 380  
 Ser Pro Leu Leu Asp His Asp Asn Ala Val Tyr Val Phe Met Gly Ala  
 385 390 395 400  
 Gly Asp Ile Gln Thr Tyr Glu Tyr Ser Phe Glu Arg Leu Leu Ser Asn  
 405 410 415  
 Leu Thr Ser Asn Val Gln  
 420

## (2) INFORMATION FOR SEQ ID NO: 117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

TTTAAACCCA ACTGTTGGTA CTTTCCTTTT TACTGCAGGA TTGAGCTTGT TAGTTTTATT

60

09765272.012201

GGTTTCTAAA	AGGGAAAATG	GAAAGAAACG	ACTTGTTTCAT	TTTCTGCTGT	TGACTAGCAT	120
GGGAGTTCAA	TTGTTGCCGG	CCAGTGCTTT	TGGGTTGACC	AGCCAGATTT	TATCTGCCTA	180
TAATAGTCAG	CTTTCTATCG	GAGTCGGGGA	ACATTTACCA	GAGCCTCTGA	AAATCGAAGG	240
TTATCAATAT	ATTGGTTATA	TCAAAACTAA	GAAACAGGAT	AATACAGAGC	TTTCAAGGAC	300
AGTTGATGGG	AAATACTCTG	CTCAAAGAGA	TAGTCAACCA	AACTCTACAA	AAACATCAGA	360
TGTAGTTCAT	TCAGCTGATT	TAGAATGGAA	CCAAGGACAG	GGGAAGGTTA	GTTTACAAGG	420
TGAAGCATCA	GGGGATGATG	GACTTTTCAGA	AAAATCTTCT	ATAGCAGCAG	ACAATCTATC	480
TTCTAATGAT	TCATTCGCAA	GTCAAGTTGA	GCAGAATCCG	GATCACAAAG	GAGAATCTGT	540
AGTTCGACCA	ACAGTGCCAG	AACAAGGAAA	TCCTGTGTCT	GCTACAACGG	TGCAGAGTGC	600
GGAAGAGGAA	GTATTGGCGA	CGACAAATGA	TCGACCAGAG	TATAAACTTC	CATTGGAAAC	660
CAAAGGCACG	CAAGAACCCG	GTCATGAGGG	TGAAGCCGCA	GTCCGTGAAG	ACTTACCAGT	720
CTACACTAAG	CCACTAGAAA	CCAAAGGTAC	ACAAGGACCC	GGACATGAAG	GTGAAGCTGC	780
AGTTCGCGAG	GAAGAACCAG	CTTACACAGA	ACCGTTAGCA	ACGAAAGGCA	CGCAAGAGCC	840
AGGTCATGAG	GGCAAAGCTA	CAGTCCGCGA	AGAGACTCTA	GAGTACACGG	AACCGGTAGC	900
GACAAAAGGC	ACACAAGAAC	CCGAACATGA	GGGCGAaCGG	SCAGTAGAAG	AAGAACTTCC	960
GGCTTTAGAG	GTCACTACAC	GAAATAGAAC	GGAAATCCAG	AATATTCCTT	ATACAACAGA	1020
AGAAATTCAG	GATCCAACAC	TTCTGAAAAA	TCGTCGTAAG	ATTGAACGAC	AAGGGCAAGC	1080
AGGGACACGT	ACAATTCAAT	ATGAAGACTA	CATCGTAAAT	GGTAATGTCG	TAGAAACTAA	1140
AGAAGTGTC	CGAACTGAAG	TAGCTCCGGT	CAACGAAGTC	GTTAAAGTAG	GAACACTTGT	1200
GAAAGTTAAA	CCTACAGTAG	AAATTACAAA	CTTAACAAAA	GTTGAGAACA	AAAAATCTAT	1260
AACTGTAAGT	TATAACTTAA	TAGACACTAC	CTCAGCATAT	GTTTCTGCAA	AAACGCAAGT	1320
TTTCCATGGA	GACAAGCTAG	TTAAAGAGGT	GGATATAGAA	AATCCTGCCA	AAGAGCAAGT	1380
AATATCAGGT	TTAGATTACT	ACACACCGTA	TACAGTTAAA	ACACACCTAA	CTTATAATTT	1440
GGGTGAAAAT	AATGAGGAAA	ATACTGAAAC	ATCAACTCAA	GATTTCCAAT	TAGAGTATAA	1500
GAAAATAGAG	ATTAAAGATA	TTGATTTCAGT	AGAATTATAC	GGTAAAGAAA	ATGATCGTTA	1560
TCGTAGATAT	TTAAGTCTAA	GTGAAGCGCC	GACTGATACG	GCTAAATACT	TTGTAAAAGT	1620
GAAATCAGAT	CGCTTCAAAG	AAATGTACCT	ACCTGTAAAA	TCTATTACAG	AAAATACGGA	1680
TGGAACGTAT	AAAGTGACGG	TAGCCGTTGA	TCAACTTGTC	GAAGAAGGTA	CAGACGGTTA	1740
CAAAGATGAT	TACACATTTA	CTGTAGCTAA	ATCTAAAGCA	GAGCAACCAG	GAGTTTACAC	1800
ATCCTTTAAA	CAGCTGGTAA	CAGCCATGCA	AAGCAATCTG	TCTGGTGTCT	ATACATTGGC	1860
TTCAGATATG	ACCGCAGATG	AGGTGAGCTT	AGGCGATAAG	CAGACAAGTT	ATCTCACAGG	1920

09765272.012201

TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT 1980  
 GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAAAC 2040  
 TGTTTCTGCT GATAGTAAAG AAAATGTGCG AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA 2100  
 TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT 2160  
 AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA 2220  
 TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG 2280  
 TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA 2340  
 CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT 2400  
 TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC 2460  
 TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA 2520  
 TGTTCATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA 2580  
 TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT 2640  
 TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT 2700  
 AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG 2760  
 CAACATAGAA AAATGATGC CATTCTACAA TAAAGACCTA GTAGTTCACT ATGGTAACAA 2820  
 AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTGA GATGTTGTGC CGATGAAAGA 2880  
 TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA 2940  
 TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAAACAG 3000  
 TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT 3060  
 TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA 3120  
 C 3121

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu  
 1 5 10 15

Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val  
 20 25 30

His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser  
 35 40 45

09765272.012201

Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu  
 50 55 60  
 Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly  
 65 70 75 80  
 Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu  
 85 90 95  
 Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln  
 100 105 110  
 Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu  
 115 120 125  
 Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly  
 130 135 140  
 Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser  
 145 150 155 160  
 Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys  
 165 170 175  
 Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val  
 180 185 190  
 Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr  
 195 200 205  
 Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln  
 210 215 220  
 Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val  
 225 230 235 240  
 Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu  
 245 250 255  
 Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu  
 260 265 270  
 Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val  
 275 280 285  
 Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr  
 290 295 300  
 Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro  
 305 310 315 320  
 Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro  
 325 330 335  
 Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg  
 340 345 350  
 Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu  
 355 360 365  
 Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg  
 370 375 380

09765272.012201

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val  
 385 390 395 400  
 Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn  
 405 410 415  
 Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala  
 420 425 430  
 Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys  
 435 440 445  
 Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu  
 450 455 460  
 Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu  
 465 470 475 480  
 Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln  
 485 490 495  
 Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu  
 500 505 510  
 Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg Tyr Leu Ser Leu Ser Glu  
 515 520 525  
 Ala Pro Thr Asp Thr Ala Lys Tyr Phe Val Lys Val Lys Ser Asp Arg  
 530 535 540  
 Phe Lys Glu Met Tyr Leu Pro Val Lys Ser Ile Thr Glu Asn Thr Asp  
 545 550 555 560  
 Gly Thr Tyr Lys Val Thr Val Ala Val Asp Gln Leu Val Glu Glu Gly  
 565 570 575  
 Thr Asp Gly Tyr Lys Asp Asp Tyr Thr Phe Thr Val Ala Lys Ser Lys  
 580 585 590  
 Ala Glu Gln Pro Gly Val Tyr Thr Ser Phe Lys Gln Leu Val Thr Ala  
 595 600 605  
 Met Gln Ser Asn Leu Ser Gly Val Tyr Thr Leu Ala Ser Asp Met Thr  
 610 615 620  
 Ala Asp Glu Val Ser Leu Gly Asp Lys Gln Thr Ser Tyr Leu Thr Gly  
 625 630 635 640  
 Ala Phe Thr Gly Ser Leu Ile Gly Ser Asp Gly Thr Lys Ser Tyr Ala  
 645 650 655  
 Ile Tyr Asp Leu Lys Lys Pro Leu Phe Asp Thr Leu Asn Gly Ala Thr  
 660 665 670  
 Val Arg Asp Leu Asp Ile Lys Thr Val Ser Ala Asp Ser Lys Glu Asn  
 675 680 685  
 Val Ala Ala Leu Ala Lys Ala Ala Asn Ser Ala Asn Ile Asn Asn Val  
 690 695 700  
 Ala Val Glu Gly Lys Ile Ser Gly Ala Lys Ser Val Ala Gly Leu Val  
 705 710 715 720

09765272 012201

Ala Ser Ala Thr Asn Thr Val Ile Glu Asn Ser Ser Phe Thr Gly Lys  
 725 730 735  
 Leu Ile Ala Asn His Gln Asp Ser Asn Lys Asn Asp Thr Gly Gly Ile  
 740 745 750  
 Val Gly Asn Ile Thr Gly Asn Ser Ser Arg Val Asn Lys Val Arg Val  
 755 760 765  
 Asp Ala Leu Ile Ser Thr Asn Ala Arg Asn Asn Asn Gln Thr Ala Gly  
 770 775 780  
 Gly Ile Val Gly Arg Leu Glu Asn Gly Ala Leu Ile Ser Asn Ser Val  
 785 790 795 800  
 Ala Thr Gly Glu Ile Arg Asn Gly Gln Gly Tyr Ser Arg Val Gly Gly  
 805 810 815  
 Ile Val Gly Ser Thr Trp Gln Asn Gly Arg Val Asn Asn Val Val Ser  
 820 825 830  
 Asn Val Asp Val Gly Asp Gly Tyr Val Ile Thr Gly Asp Gln Tyr Ala  
 835 840 845  
 Ala Ala Asp Val Lys Asn Ala Ser Thr Ser Val Asp Asn Arg Lys Ala  
 850 855 860  
 Asp Arg Phe Ala Thr Lys Leu Ser Lys Asp Gln Ile Asp Ala Lys Val  
 865 870 875 880  
 Ala Asp Tyr Gly Ile Thr Val Thr Leu Asp Asp Thr Gly Gln Asp Leu  
 885 890 895  
 Lys Arg Asn Leu Arg Glu Val Asp Tyr Thr Arg Leu Asn Lys Ala Glu  
 900 905 910  
 Ala Glu Arg Lys Val Ala Tyr Ser Asn Ile Glu Lys Leu Met Pro Phe  
 915 920 925  
 Tyr Asn Lys Asp Leu Val Val His Tyr Gly Asn Lys Val Ala Thr Thr  
 930 935 940  
 Asp Lys Leu Tyr Thr Thr Glu Leu Leu Asp Val Val Pro Met Lys Asp  
 945 950 955 960  
 Asp Glu Val Val Thr Asp Ile Asn Asn Lys Lys Asn Ser Ile Asn Lys  
 965 970 975  
 Val Met Leu His Phe Lys Asp Asn Thr Val Glu Tyr Leu Asp Val Thr  
 980 985 990  
 Phe Lys Glu Asn Phe Ile Asn Ser Gln Val Ile Glu Tyr Asn Val Thr  
 995 1000 1005  
 Gly Lys Glu Tyr Ile Phe Thr Pro Glu Ala Phe Val Ser Asp Tyr Thr  
 1010 1015 1020  
 Ala Ile Thr Asn Asn Val Leu Ser Asp Leu Gln Asn Val Thr Leu Asn  
 1025 1030 1035 1040



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TTTTAACCCA	ACTGTTGGTA	CTTTCCTTTT	TACTGCAGGA	TTGAGCTTGT	TAGTTTTATT	60
GGTTTCTAAA	AGGGAAAATG	GAAAGAAACG	ACTTGTTTCAT	TTTCTGCTGT	TGACTAGCAT	120
GGGAGTTCAA	TTGTTGCCGG	CCAGTGCTTT	TGGGTTGACC	AGCCAGATTT	TATCTGCCTA	180
TAATAGTCAG	CTTTCATCG	GAGTCGGGGA	ACATTTACCA	GAGCCTCTGA	AAATCGAAGG	240
TTATCAATAT	ATTGGTTATA	TCAAACTAA	GAAACAGGAT	AATACAGAGC	TTTCAAGGAC	300
AGTTGATGGG	AAATACTCTG	CTCAAAGAGA	TAGTCAACCA	AACTCTACAA	AAACATCAGA	360
TGTAGTTCAT	TCAGCTGATT	TAGAATGGAA	CCAAGGACAG	GGGAAGGTTA	GTTTACAAGG	420
TGAAGCATCA	GGGGATGATG	GACTTTCAGA	AAAATCTTCT	ATAGCAGCAG	ACAATCTATC	480
TTCTAATGAT	TCATTGCAA	GTCAAGTTGA	GCAGAATCCG	GATCACAAAG	GAGAATCTGT	540
AGTTCGACCA	ACAGTGCCAG	AACAAGGAAA	TCCTGTGTCT	GCTACAACGG	TGCAGAGTGC	600
GGAAGAGGAA	GTATTGGCGA	CGACAAATGA	TCGACCAGAG	TATAAACTTC	CATTGGAAAC	660
CAAAGGCACG	CAAGAACCCG	GTCATGAGGG	TGAAGCCGCA	GTCCGTGAAG	ACTTACCAGT	720
CTACACTAAG	CCACTAGAAA	CCAAAGGTAC	ACAAGGACCC	GGACATGAAG	GTGAAGCTGC	780
AGTTCGCGAG	GAAGAACCAG	CTTACACAGA	ACCGTTAGCA	ACGAAAGGCA	CGCAAGAGCC	840
AGGTCATGAG	GGCAAAGCTA	CAGTCCGCGA	AGAGACTCTA	GAGTACACGG	AACCGGTAGC	900
GACAAAAGGC	ACACAAGAAC	CCGAACATGA	GGGCGAaCGG	sCAGTAGAAG	AAGAACTTCC	960
GGCTTTAGAG	GTCACTACAC	GAAATAGAAC	GGAAATCCAG	AATATTCCTT	ATACAACAGA	1020
AGAAATTCAG	GATCCAACAC	TTCTGAAAAA	TCGTCGTAAG	ATTGAACGAC	AAGGGCAAGC	1080
AGGGACACGT	ACAATTCAAT	ATGAAGACTA	CATCGTAAAT	GGTAATGTCT	TAGAAACTAA	1140
AGAAGTGTC	CGAACTGAAG	TAGCTCCGGT	CAACGAAGTC	GTTAAAGTAG	GAACACTTGT	1200
GAAAGTTAAA	CCTACAGTAG	AAATTACAAA	CTTAACAAAA	GTTGAGAACA	AAAAATCTAT	1260
AACTGTAAGT	TATAACTTAA	TAGACACTAC	CTCAGCATAT	GTTTCTGCAA	AAACGCAAGT	1320
TTTCCATGGA	GACAAGCTAG	TTAAAGAGGT	GGATATAGAA	AATCCTGCCA	AAGAGCAAGT	1380
AATATCAGGT	TTAGATTACT	ACACACCGTA	TACAGTTAAA	ACACACCTAA	CTTATAATTT	1440
GGGTGAAAAT	AATGAGGAAA	ATACTGAAAC	ATCAACTCAA	GATTTCCAAT	TAGAGTATAA	1500
GAAAATAGAG	ATTAAAGATA	TTGATTCAGT	AGAATTATAC	GGTAAAGAAA	ATGATCGTTA	1560
TCGTAGA						1567

09765272.012201

## (2) INFORMATION FOR SEQ ID NO:120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu
1          5          10          15

Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val
          20          25          30

His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser
          35          40          45

Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu
          50          55          60

Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly
65          70          75          80

Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu
          85          90          95

Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln
          100          105          110

Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu
          115          120          125

Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly
          130          135          140

Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser
145          150          155          160

Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys
          165          170          175

Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val
          180          185          190

Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr
          195          200          205

Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln
          210          215          220

Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val
225          230          235          240

Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu
          245          250          255

Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu

```

09765272.012201

236

260

265

270

Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val  
275 280 285

Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr  
290 295 300

Gln Glu Pro Glu His Glu Gly Glu Arg Xaa Val Glu Glu Glu Leu Pro  
305 310 315 320

Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro  
325 330 335

Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg  
340 345 350

Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu  
355 360 365

Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg  
370 375 380

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val  
385 390 395 400

Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn  
405 410 415

Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala  
420 425 430

Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys  
435 440 445

Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu  
450 455 460

Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu  
465 470 475 480

Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln  
485 490 495

Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu  
500 505 510

Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg  
515 520

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1561 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121: .....

TCGTAGATAT TTAAGTCTAA GTGAAGCGCC GACTGATACG GCTAAATACT TTGTAAAAGT

60

09765272.012201

09765272 "012201"

GAAATCAGAT CGCTTCAAAG AAATGTACCT ACCTGTAAAA TCTATTACAG AAAATACGGA	120
TGGAACGTAT AAAGTGACGG TAGCCGTTGA TCAACTTGTC GAAGAAGGTA CAGACGGTTA	180
CAAAGATGAT TACACATTTA CTGTAGCTAA ATCTAAAGCA GAGCAACCAG GAGTTTACAC	240
ATCCTTTAAA CAGCTGGTAA CAGCCATGCA AAGCAATCTG TCTGGTGTCT ATACATTGGC	300
TTCAGATATG ACCGCAGATG AGGTGAGCTT AGGCGATAAG CAGACAAGTT ATCTCACAGG	360
TGCATTTACA GGGAGCTTGA TCGGTTCTGA TGGAACAAAA TCGTATGCCA TTTATGATTT	420
GAAGAAACCA TTATTTGATA CATTAAATGG TGCTACAGTT AGAGATTTGG ATATTAATAAC	480
TGTTTCTGCT GATAGTAAAG AAAATGTCGC AGCGCTGGCG AAGGCAGCGA ATAGCGCGAA	540
TATTAATAAT GTTGCAGTAG AAGGAAAAAT CTCAGGTGCG AAATCTGTTG CGGGATTAGT	600
AGCGAGCGCA ACAAATACAG TGATAGAAAA CAGCTCGTTT ACAGGGAAAC TTATCGCAAA	660
TCACCAGGAC AGTAATAAAA ATGATACTGG AGGAATAGTA GGTAATATAA CAGGAAATAG	720
TTCGAGAGTT AATAAAGTTA GGGTAGATGC CTTAATCTCT ACTAATGCAC GCAATAATAA	780
CCAAACAGCT GGAGGGATAG TAGGTAGATT AGAAAATGGT GCATTGATAT CTAATTCGGT	840
TGCTACTGGA GAAATACGAA ATGGTCAAGG ATATTCTAGA GTCGGAGGAA TAGTAGGATC	900
TACGTGGCAA AACGGTCGAG TAAATAATGT TGTGAGTAAC GTAGATGTTG GAGATGGTTA	960
TGTTATCACC GGTGATCAAT ACGCAGCAGC AGATGTGAAA AATGCAAGTA CATCAGTTGA	1020
TAATAGAAAA GCAGACAGAT TCGCTACAAA ATTATCAAAA GACCAAATAG ACGCGAAAGT	1080
TGCTGATTAT GGAATCACAG TAACTCTTGA TGATACTGGG CAAGATTTAA AACGTAATCT	1140
AAGAGAAGTT GATTATACAA GACTAAATAA AGCAGAAGCT GAAAGAAAAG TAGCTTATAG	1200
CAACATAGAA AACTGATGC CATTCTACAA TAAAGACCTA GTAGTTCAC TATGGTAACAA	1260
AGTAGCGACA ACAGATAAAC TTTACACTAC AGAATTGTTA GATGTTGTGC CGATGAAAGA	1320
TGATGAAGTA GTAACGGATA TTAATAATAA GAAAAATTCA ATAAATAAAG TTATGTTACA	1380
TTTCAAAGAT AATACAGTAG AATACCTAGA TGTAACATTC AAAGAAAAC TCATAAACAG	1440
TCAAGTAATC GAATACAATG TTACAGGAAA AGAATATATA TTCACACCAG AAGCATTTGT	1500
TTCAGACTAT ACAGCGATAA CGAATAACGT ACTAAGCGAC TTGCAAAATG TAACACTTAA	1560
C	1561

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Arg	Arg	Tyr	Leu	Ser	Leu	Ser	Glu	Ala	Pro	Thr	Asp	Thr	Ala	Lys	Tyr	1	5	10	15
Phe	Val	Lys	Val	Lys	Ser	Asp	Arg	Phe	Lys	Glu	Met	Tyr	Leu	Pro	Val	20	25	30	
Lys	Ser	Ile	Thr	Glu	Asn	Thr	Asp	Gly	Thr	Tyr	Lys	Val	Thr	Val	Ala	35	40	45	
Val	Asp	Gln	Leu	Val	Glu	Glu	Gly	Thr	Asp	Gly	Tyr	Lys	Asp	Asp	Tyr	50	55	60	
Thr	Phe	Thr	Val	Ala	Lys	Ser	Lys	Ala	Glu	Gln	Pro	Gly	Val	Tyr	Thr	65	70	75	80
Ser	Phe	Lys	Gln	Leu	Val	Thr	Ala	Met	Gln	Ser	Asn	Leu	Ser	Gly	Val	85	90	95	
Tyr	Thr	Leu	Ala	Ser	Asp	Met	Thr	Ala	Asp	Glu	Val	Ser	Leu	Gly	Asp	100	105	110	
Lys	Gln	Thr	Ser	Tyr	Leu	Thr	Gly	Ala	Phe	Thr	Gly	Ser	Leu	Ile	Gly	115	120	125	
Ser	Asp	Gly	Thr	Lys	Ser	Tyr	Ala	Ile	Tyr	Asp	Leu	Lys	Lys	Pro	Leu	130	135	140	
Phe	Asp	Thr	Leu	Asn	Gly	Ala	Thr	Val	Arg	Asp	Leu	Asp	Ile	Lys	Thr	145	150	155	160
Val	Ser	Ala	Asp	Ser	Lys	Glu	Asn	Val	Ala	Ala	Leu	Ala	Lys	Ala	Ala	165	170	175	
Asn	Ser	Ala	Asn	Ile	Asn	Asn	Val	Ala	Val	Glu	Gly	Lys	Ile	Ser	Gly	180	185	190	
Ala	Lys	Ser	Val	Ala	Gly	Leu	Val	Ala	Ser	Ala	Thr	Asn	Thr	Val	Ile	195	200	205	
Glu	Asn	Ser	Ser	Phe	Thr	Gly	Lys	Leu	Ile	Ala	Asn	His	Gln	Asp	Ser	210	215	220	
Asn	Lys	Asn	Asp	Thr	Gly	Gly	Ile	Val	Gly	Asn	Ile	Thr	Gly	Asn	Ser	225	230	235	240
Ser	Arg	Val	Asn	Lys	Val	Arg	Val	Asp	Ala	Leu	Ile	Ser	Thr	Asn	Ala	245	250	255	
Arg	Asn	Asn	Asn	Gln	Thr	Ala	Gly	Gly	Ile	Val	Gly	Arg	Leu	Glu	Asn	260	265	270	
Gly	Ala	Leu	Ile	Ser	Asn	Ser	Val	Ala	Thr	Gly	Glu	Ile	Arg	Asn	Gly	275	280	285	
Gln	Gly	Tyr	Ser	Arg	Val	Gly	Gly	Ile	Val	Gly	Ser	Thr	Trp	Gln	Asn	290	295	300	
Gly	Arg	Val	Asn	Asn	Val	Val	Ser	Asn	Val	Asp	Val	Gly	Asp	Gly	Tyr	305	310	315	320

09765272.012201

Val Ile Thr Gly Asp Gln Tyr Ala Ala Asp Val Lys Asn Ala Ser  
 325 330 335

Thr Ser Val Asp Asn Arg Lys Ala Asp Arg Phe Ala Thr Lys Leu Ser  
 340 345 350

Lys Asp Gln Ile Asp Ala Lys Val Ala Asp Tyr Gly Ile Thr Val Thr  
 355 360 365

Leu Asp Asp Thr Gly Gln Asp Leu Lys Arg Asn Leu Arg Glu Val Asp  
 370 375 380

Tyr Thr Arg Leu Asn Lys Ala Glu Ala Glu Arg Lys Val Ala Tyr Ser  
 385 390 395 400

Asn Ile Glu Lys Leu Met Pro Phe Tyr Asn Lys Asp Leu Val Val His  
 405 410 415

Tyr Gly Asn Lys Val Ala Thr Thr Asp Lys Leu Tyr Thr Thr Glu Leu  
 420 425 430

Leu Asp Val Val Pro Met Lys Asp Asp Glu Val Val Thr Asp Ile Asn  
 435 440 445

Asn Lys Lys Asn Ser Ile Asn Lys Val Met Leu His Phe Lys Asp Asn  
 450 455 460

Thr Val Glu Tyr Leu Asp Val Thr Phe Lys Glu Asn Phe Ile Asn Ser  
 465 470 475 480

Gln Val Ile Glu Tyr Asn Val Thr Gly Lys Glu Tyr Ile Phe Thr Pro  
 485 490 495

Glu Ala Phe Val Ser Asp Tyr Thr Ala Ile Thr Asn Asn Val Leu Ser  
 500 505 510

Asp Leu Gln Asn Val Thr Leu Asn  
 515 520

## (2) INFORMATION FOR SEQ ID NO: 123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTTTGGTTTT GAAGGAAGTA AGCGTGGACA ATTTGCTGTA GAAGGAATCA ATCAACTTCG	60
TGAGCATGTA GAACTCTAT TGATTATCTC AAACAACAAT TTGCTTGAAA TTGTTGATAA	120
GAAAACACCG CTTTGGAGG CTCTTAGCGA AGCGGATAAC GTTCTTCGTC AAGGTGTTCA	180
AGGGATTACC GATTTGATTA CCAATCCAGG ATTGATTAAC CTTGACTTTG CCGATGTGAA	240
AACGGTAATG GCAAACAAAG GGAATGCTCT TATGGGTATT GGTATCGGTA GTGGAGAAGA	300
ACGTGTGGTA GAAGCGGCAC GTAAGGCAAT CTATTCACCA CTTCTTGAAA CAACTATTGA	360

CGGTGCTGAG GATGTTATCG TCAACGTTAC TGGTGGTCTT GACTTAACCT TGATTGAGGC 420  
 AGAAGAGGCT TCACAAATTG TGAACCAGGC AGCAGGTCAA GGAGTGAACA TCTGGCTCGG 480  
 TACTTCAATT GATGAAAGTA TGC GTGATGA AATTCGTGTA ACAGTTGTTG CAACGGGTGT 540  
 TCGTCAAGAC CGCGTAGAAA AGGTTGTGGC TCCACAAGCT AGATCTGCTA CTA ACTACCG 600  
 TGAGACAGTG AAACCAGCTC ATTCACATGG CTTTGATCGT CATTTTGATA TGGCAGAAAC 660  
 AGTTGAATTG CCAAAACAAA ATCCACGTCG TTTGGAACCA ACTCAGGCAT CTGCTTTTGG 720  
 TGATTGGGAT CTTGCCCGTG AATCGATTGT TCGTACAACA GATTCAGTCG TTTCTCCAGT 780  
 CGAGCGCTTT GAAGCCCCAA TTTCACAAGA TGAAGATGAA TTGGATACAC CTCCATTTT 840  
 CAAAAATCGT 850

## (2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Phe	Gly	Phe	Glu	Gly	Ser	Lys	Arg	Gly	Gln	Phe	Ala	Val	Glu	Gly	Ile	1	5	10	15
Asn	Gln	Leu	Arg	Glu	His	Val	Asp	Thr	Leu	Leu	Ile	Ile	Ser	Asn	Asn	20	25	30	
Asn	Leu	Leu	Glu	Ile	Val	Asp	Lys	Lys	Thr	Pro	Leu	Leu	Glu	Ala	Leu	35	40	45	
Ser	Glu	Ala	Asp	Asn	Val	Leu	Arg	Gln	Gly	Val	Gln	Gly	Ile	Thr	Asp	50	55	60	
Leu	Ile	Thr	Asn	Pro	Gly	Leu	Ile	Asn	Leu	Asp	Phe	Ala	Asp	Val	Lys	65	70	75	80
Thr	Val	Met	Ala	Asn	Lys	Gly	Asn	Ala	Leu	Met	Gly	Ile	Gly	Ile	Gly	85	90	95	
Ser	Gly	Glu	Glu	Arg	Val	Val	Glu	Ala	Ala	Arg	Lys	Ala	Ile	Tyr	Ser	100	105	110	
Pro	Leu	Leu	Glu	Thr	Thr	Ile	Asp	Gly	Ala	Glu	Asp	Val	Ile	Val	Asn	115	120	125	
Val	Thr	Gly	Gly	Leu	Asp	Leu	Thr	Leu	Ile	Glu	Ala	Glu	Glu	Ala	Ser	130	135	140	
Gln	Ile	Val	Asn	Gln	Ala	Ala	Gly	Gln	Gly	Val	Asn	Ile	Trp	Leu	Gly	145	150	155	160
Thr	Ser	Ile	Asp	Glu	Ser	Met	Arg	Asp	Glu	Ile	Arg	Val	Thr	Val	Val	165	170	175	

09765272.012201

Ala Thr Gly Val Arg Gln Asp Arg Val Glu Lys Val Val Ala Pro Gln  
180 185 190

Ala Arg Ser Ala Thr Asn Tyr Arg Glu Thr Val Lys Pro Ala His Ser  
195 200 205

His Gly Phe Asp Arg His Phe Asp Met Ala Glu Thr Val Glu Leu Pro  
210 215 220

Lys Gln Asn Pro Arg Arg Leu Glu Pro Thr Gln Ala Ser Ala Phe Gly  
225 230 235 240

Asp Trp Asp Leu Arg Arg Glu Ser Ile Val Arg Thr Thr Asp Ser Val  
245 250 255

Val Ser Pro Val Glu Arg Phe Glu Ala Pro Ile Ser Gln Asp Glu Asp  
260 265 270

Glu Leu Asp Thr Pro Pro Phe Phe Lys Asn Arg  
275 280

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CTACTACCTC TCGAGAGAAA GTGACCTAGA GGTGACCGTT TTTGACCATG AGCAAGGTCA	60
AGCCACCAAG GCCGCAGCAG GAATTATCAG TCCTTGTTT TCCAAACGCC GTAATAAAGC	120
CTGGTACAAG ATGGCGCGCT TGGGGGCTGA TTTTATGTG GATTTATTAG CTGATTTAGA	180
GAAATCAGGA CAAGAAATCG ACTTTTACCA GCGTTCGGGA GTCTTTCTCT TGAAAAAGGA	240
TGAATCCAAT TTGGAAGAAC TTTATCAACT GGCCCTCCAG CGCAGAGAAG AATCTCCCTT	300
GATAGGGCAA TTAGCCATTC TGAACCAAGC CTCAGCTAAT GAATTATTCC CTGGTTTGCA	360
GGGATTTGAC CGCCTGCTCT ATGCTTCTGG TGGAGCGAGA GTAGATGGCC AACTTTTAGT	420
GACTCGTTTG CTGGAAGTCA GTCATGTCAA GCTGGTCAAA GAAAAAGTGA CTCTGACACC	480
GTTAGCATCA GGCTACCAGA TTGGTGAAGA GGAGTTTGAG CAGGTTATTT TGGCGACGGG	540
AGCTTGGTTG GGGGACATGT TAGAGCCTTT AGGTTATGAA GTGGATGTCC GTCCTCAAAA	600
AGGACAACTA CGAGATTATC AGCTTGCCCA AGACATGGAA GATTACCCTG TTGTCATGCC	660
AGAAGGGGAG TGGGATTGGA TTCCCTTTGC AGGTGGGAAA TTATCCTTAG GCGCTACCCA	720
CGAAAATGAC ATGGGATTTG ATTTGACGGT AGATGAAACC TTGCTCCAAC AAATGGAGGA	780
GGCCACCTTG ACTCACTATC TGATTTTGGC TGAAGCTACT TCAAAATCTG AGCGTGTTGG	840
AATCCGTGCC TACACCAGTG ATTTCTCTCC TTTCTTTGGG CAGGTGCCTG ACTTAACTGG	900



TGTCTATGCA GCCAGTGGAC TAGGTTTCATC AGGCTCACA ACTGGTCCTA TCATTGGTTA 960  
 CCATCTAGCC CAACTGATCC AAGACAAGGA GTTGACCTTG GACCCTCTAA ATTACCCAAT 1020  
 TGAAAACTAT GTCAAACGAG TAAAAAGCGA A 1051

## (2) INFORMATION FOR SEQ ID NO:126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Tyr	Tyr	Leu	Ser	Arg	Glu	Ser	Asp	Leu	Glu	Val	Thr	Val	Phe	Asp	His	1	5	10	15
Glu	Gln	Gly	Gln	Ala	Thr	Lys	Ala	Ala	Ala	Gly	Ile	Ile	Ser	Pro	Trp	20	25	30	
Phe	Ser	Lys	Arg	Arg	Asn	Lys	Ala	Trp	Tyr	Lys	Met	Ala	Arg	Leu	Gly	35	40	45	
Ala	Asp	Phe	Tyr	Val	Asp	Leu	Leu	Ala	Asp	Leu	Glu	Lys	Ser	Gly	Gln	50	55	60	
Glu	Ile	Asp	Phe	Tyr	Gln	Arg	Ser	Gly	Val	Phe	Leu	Leu	Lys	Lys	Asp	65	70	75	80
Glu	Ser	Asn	Leu	Glu	Glu	Leu	Tyr	Gln	Leu	Ala	Leu	Gln	Arg	Arg	Glu	85	90	95	
Glu	Ser	Pro	Leu	Ile	Gly	Gln	Leu	Ala	Ile	Leu	Asn	Gln	Ala	Ser	Ala	100	105	110	
Asn	Glu	Leu	Phe	Pro	Gly	Leu	Gln	Gly	Phe	Asp	Arg	Leu	Leu	Tyr	Ala	115	120	125	
Ser	Gly	Gly	Ala	Arg	Val	Asp	Gly	Gln	Leu	Leu	Val	Thr	Arg	Leu	Leu	130	135	140	
Glu	Val	Ser	His	Val	Lys	Leu	Val	Lys	Glu	Lys	Val	Thr	Leu	Thr	Pro	145	150	155	160
Leu	Ala	Ser	Gly	Tyr	Gln	Ile	Gly	Glu	Glu	Glu	Phe	Glu	Gln	Val	Ile	165	170	175	
Leu	Ala	Thr	Gly	Ala	Trp	Leu	Gly	Asp	Met	Leu	Glu	Pro	Leu	Gly	Tyr	180	185	190	
Glu	Val	Asp	Val	Arg	Pro	Gln	Lys	Gly	Gln	Leu	Arg	Asp	Tyr	Gln	Leu	195	200	205	
Ala	Gln	Asp	Met	Glu	Asp	Tyr	Pro	Val	Val	Met	Pro	Glu	Gly	Glu	Trp	210	215	220	
Asp	Leu	Ile	Pro	Phe	Ala	Gly	Gly	Lys	Leu	Ser	Leu	Gly	Ala	Thr	His				

09765272.012204

(2) INFORMATION FOR SEQ ID NO: 127:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

(2) INFORMATION FOR SEQ ID NO:128:

(ii) MOLECULE TYPE: protein

Lys Val Lys Ser Gln Thr Ala Lys Lys Val Leu Glu Lys Ile Gly Ala  
1 5 10 15

244

Asp Ser Val Ile Ser Pro Glu Tyr Glu Met Gly Gln Ser Leu Ala Gln  
 20 25 30  
 Thr Ile Leu Phe His Asn Ser Val Asp Val Phe Gln Leu Asp Lys Asn  
 35 40 45  
 Val Ser Ile Val Glu Met Lys Ile Pro Gln Ser Trp Ala Gly Gln Ser  
 50 55 60  
 Leu Ser Lys Leu Asp Leu Arg Gly Lys Tyr Asn Leu Asn Ile Leu Gly  
 65 70 75 80  
 Phe Arg Glu Gln Glu Asn Ser Pro Leu Asp Val Glu Phe Gly Pro Asp  
 85 90 95  
 Asp Leu Leu Lys Ala Asp Thr Tyr Ile Leu Ala Val Ile Asn Asn Gln  
 100 105 110  
 Tyr Leu Asp Thr Leu  
 115

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 247 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGACGGGTCT CAGGATCAGA CTCAGGAAAT CGCTGAGTGT TTAGCTAGCA AGTATCCTAA	60
TATCGTTAGA GCCATCTATC AGGAAAATAA ATGCCATGGC GGTGCGGTCA ATCGTGGCTT	120
GGTAGAGGCT TCTGGGCGCT ATTTTAAAGT AGTTGACAGT GATGACTGGG TGGATCCTCG	180
TGCCTACTTG AAAATTCTTG AACTTGCAG GAACTTGAGA GCAAAGGTCA AGAGGTGGAT	240
GTCTTTG	247

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Gly Ser Gln Asp Gln Thr Gln Glu Ile Ala Glu Cys Leu Ala Ser  
 1 5 10 15  
 Lys Tyr Pro Asn Ile Val Arg Ala Ile Tyr Gln Glu Asn Lys Cys His  
 20 25 30  
 Gly Gly Ala Val Asn Arg Gly Leu Val Glu Ala Ser Gly Arg Tyr Phe

09765272 012201

35

40

45

Lys Val Val Asp Ser Asp Asp Trp Val Asp Pro Arg Ala Tyr Leu Lys  
50 55 60

Ile Leu Glu Thr Cys Arg Asn Leu Arg Ala Lys Val Lys Arg Trp Met  
65 70 75 80

Ser Leu

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

TAGAGGCTTT GCCAAATGGT GGAAGGGCA CGAGCGTCGA AAAGAGGAAC GCTTTGTCAA	60
ACAAGAAGAA AAAGCTCGCC AAAAGGCTGA GAAAGAGGCT AGATTAGAAC AAGAAGAGAC	120
TGAAAAAGCC TTA CTGATT TGCCTCCTGT TGATATGGAA ACGGGTGAAA TTCTGACAGA	180
GGAAGCTGTT CAAAATCTTC CACCTATTCC AGAAGAAAAG TGGGTGGAAC CAGAAATCAT	240
CCTGCCTCAA GCTGAACTTA AATTCCTGA ACAGGAAGAT GACTCAGATG ACGAAGATGT	300
TCAGGTCGAT TTTTCAGCCA AAGAAGCCCT TGAATACAAA CTTCCAAGCT TACAACTCTT	360
TGCACCAGAT AAACCAAAAG ATCAGTCTAA AGAGAAGAAA ATTGTCAGAG AAAATATCAA	420
AATCTTAGAA GCAACCTTTG CTAGCTTTGG TATTAAGGTA ACAGTTGAAC GGGCCGAAAT	480
TGGGCCATCA GTGACCAAGT ATGAAGTCAA GCCGGCTGTT GGTGTAAGGG TCAACCGCAT	540
TTCCAATCTA TCAGATGACC TCGCTCTAGC CTTGGCTGCC AAAGATGTCC GGATTGAAGC	600
ACCAATCCCT GGGAAATCCC TAATCGGAAT TGAAGTGCCC AACTCCGATA TTGCCACTGT	660
ATCTTTCCGA GAACTATGGG AACAATCGCA AACGAAAGCA GAAAATTTCT TGGAAATTCC	720
TTTAGGGAAG GCTGTTAATG GAACCGCAAG AGCTTTTGAC CTTTCTAAAA TGCCCCACTT	780
GCTAGTTGCA GGTTCACGG GTTCAGGGAA GTCAGTAGCA GTTAACGGCA TTATTGCTAG	840
CATTCTCATG AAGGCGAGAC CAGATCAAGT TAAATTTATG ATGGTCGATC CCAAGATGGT	900
TGAGTTATCT GTTTACAATG ATATTCCCCA CCTCTTGATT CCAGTCGTGA CCAATCCACG	960
CAAAGCCAGC AAGGCTCTGC AAAAGGTTGT GGATGAAATG GAAAACCGTT ATGAACTCTT	1020
TGCCAAGGTG GGAGTTCGGA ATATTGCAGG TTTTAATGCC AAGGTAGAAG AGTTCAATTC	1080
CCAGTCTGAG TACAAGCAAA TTCCGCTACC ATTCATTGTC GTGATTGTGG ATGAGTTGGC	1140
TGACCTCATG ATGGTGGCCA GCAAGGAAGT GGAAGATGCT ATCATCCGTC TTGGGCAGAA	1200

09765272.012201

GGCGCGTGCT GCAGGTATCC ACATGATTCT TGCAACTCAG CGTCCATCTG TTGATGTCAT 1260  
 CTCTGGTTTG ATTAAGGCCA ATGTTCCATC TCGTGTAGCA TTTGCGGTTT CATCAGGAAC 1320  
 AGACTCCCGT ACGATTTTGG ATGAAAATGG AGCAGAAAAA CTTCTTGGTC GAGGAGACAT 1380  
 GCTCTTTAAA CCGATTGATG AAAATCATCC AGTTCGTCTC CAAGGCTCCT TTATCTCGGA 1440  
 TGACGATGTT GAGCGCATTG TGAAC TTCAT CAAGACTCAG GCAGATGCAG ACTACGATGA 1500  
 GAGTTTTGAT CCAGGTGAGG TTTCTGAAAA TGAAGGAGAA TTTTCGGATG GAGATGCTGG 1560  
 TGGTGATCCG CTTTTTGAAG AAGCTAAGTC TTTGGTTATC GAAACACAGA AAGCCAGTGC 1620  
 GTCTATGATT CAGCGTCGTT TATCAGTTGG ATTTAACCGT GCGACCCGTC TCATGGAAGA 1680  
 ACTGGAGATA GCAGGTGTCA TCGGTCCAGC TGAAGGTACC AAACCTCGAA AAGTGTTACA 1740  
 ACAA 1744

## (2) INFORMATION FOR SEQ ID NO:132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Arg	Gly	Phe	Ala	Lys	Trp	Trp	Glu	Gly	His	Glu	Arg	Arg	Lys	Glu	Glu	1	5	10	15
Arg	Phe	Val	Lys	Gln	Glu	Glu	Lys	Ala	Arg	Gln	Lys	Ala	Glu	Lys	Glu	20	25	30	
Ala	Arg	Leu	Glu	Gln	Glu	Glu	Thr	Glu	Lys	Ala	Leu	Leu	Asp	Leu	Pro	35	40	45	
Pro	Val	Asp	Met	Glu	Thr	Gly	Glu	Ile	Leu	Thr	Glu	Glu	Ala	Val	Gln	50	55	60	
Asn	Leu	Pro	Pro	Ile	Pro	Glu	Glu	Lys	Trp	Val	Glu	Pro	Glu	Ile	Ile	65	70	75	80
Leu	Pro	Gln	Ala	Glu	Leu	Lys	Phe	Pro	Glu	Gln	Glu	Asp	Asp	Ser	Asp	85	90	95	
Asp	Glu	Asp	Val	Gln	Val	Asp	Phe	Ser	Ala	Lys	Glu	Ala	Leu	Glu	Tyr	100	105	110	
Lys	Leu	Pro	Ser	Leu	Gln	Leu	Phe	Ala	Pro	Asp	Lys	Pro	Lys	Asp	Gln	115	120	125	
Ser	Lys	Glu	Lys	Lys	Ile	Val	Arg	Glu	Asn	Ile	Lys	Ile	Leu	Glu	Ala	130	135	140	
Thr	Phe	Ala	Ser	Phe	Gly	Ile	Lys	Val	Thr	Val	Glu	Arg	Ala	Glu	Ile	145	150	155	160

09765272-012201

Gly	Pro	Ser	Val	Thr	Lys	Tyr	Glu	Val	Lys	Pro	Ala	Val	Gly	Val	Arg		
				165					170					175			
Val	Asn	Arg	Ile	Ser	Asn	Leu	Ser	Asp	Asp	Leu	Ala	Leu	Ala	Leu	Ala		
			180					185						190			
Ala	Lys	Asp	Val	Arg	Ile	Glu	Ala	Pro	Ile	Pro	Gly	Lys	Ser	Leu	Ile		
		195					200					205					
Gly	Ile	Glu	Val	Pro	Asn	Ser	Asp	Ile	Ala	Thr	Val	Ser	Phe	Arg	Glu		
	210					215					220						
Leu	Trp	Glu	Gln	Ser	Gln	Thr	Lys	Ala	Glu	Asn	Phe	Leu	Glu	Ile	Pro		
225					230					235					240		
Leu	Gly	Lys	Ala	Val	Asn	Gly	Thr	Ala	Arg	Ala	Phe	Asp	Leu	Ser	Lys		
				245					250					255			
Met	Pro	His	Leu	Leu	Val	Ala	Gly	Ser	Thr	Gly	Ser	Gly	Lys	Ser	Val		
			260					265					270				
Ala	Val	Asn	Gly	Ile	Ile	Ala	Ser	Ile	Leu	Met	Lys	Ala	Arg	Pro	Asp		
		275					280					285					
Gln	Val	Lys	Phe	Met	Met	Val	Asp	Pro	Lys	Met	Val	Glu	Leu	Ser	Val		
	290					295					300						
Tyr	Asn	Asp	Ile	Pro	His	Leu	Leu	Ile	Pro	Val	Val	Thr	Asn	Pro	Arg		
305					310					315					320		
Lys	Ala	Ser	Lys	Ala	Leu	Gln	Lys	Val	Val	Asp	Glu	Met	Glu	Asn	Arg		
				325					330					335			
Tyr	Glu	Leu	Phe	Ala	Lys	Val	Gly	Val	Arg	Asn	Ile	Ala	Gly	Phe	Asn		
		340					345						350				
Ala	Lys	Val	Glu	Glu	Phe	Asn	Ser	Gln	Ser	Glu	Tyr	Lys	Gln	Ile	Pro		
		355					360					365					
Leu	Pro	Phe	Ile	Val	Val	Ile	Val	Asp	Glu	Leu	Ala	Asp	Leu	Met	Met		
	370					375					380						
Val	Ala	Ser	Lys	Glu	Val	Glu	Asp	Ala	Ile	Ile	Arg	Leu	Gly	Gln	Lys		
385					390					395					400		
Ala	Arg	Ala	Ala	Gly	Ile	His	Met	Ile	Leu	Ala	Thr	Gln	Arg	Pro	Ser		
				405					410					415			
Val	Asp	Val	Ile	Ser	Gly	Leu	Ile	Lys	Ala	Asn	Val	Pro	Ser	Arg	Val		
			420					425					430				
Ala	Phe	Ala	Val	Ser	Ser	Gly	Thr	Asp	Ser	Arg	Thr	Ile	Leu	Asp	Glu		
		435					440					445					
Asn	Gly	Ala	Glu	Lys	Leu	Leu	Gly	Arg	Gly	Asp	Met	Leu	Phe	Lys	Pro		
	450					455					460						
Ile	Asp	Glu	Asn	His	Pro	Val	Arg	Leu	Gln	Gly	Ser	Phe	Ile	Ser	Asp		
465					470					475					480		
Asp	Asp	Val	Glu	Arg	Ile	Val	Asn	Phe	Ile	Lys	Thr	Gln	Ala	Asp	Ala		
				485					490					495			

09765272 012201

Asp Tyr Asp Glu Ser Phe Asp Pro Gly Glu Val Ser Glu Asn Glu Gly  
 500 505 510  
 Glu Phe Ser Asp Gly Asp Ala Gly Gly Asp Pro Leu Phe Glu Glu Ala  
 515 520 525  
 Lys Ser Leu Val Ile Glu Thr Gln Lys Ala Ser Ala Ser Met Ile Gln  
 530 535 540  
 Arg Arg Leu Ser Val Gly Phe Asn Arg Ala Thr Arg Leu Met Glu Glu  
 545 550 555 560  
 Leu Glu Ile Ala Gly Val Ile Gly Pro Ala Glu Gly Thr Lys Pro Arg  
 565 570 575  
 Lys Val Leu Gln Gln  
 580

## (2) INFORMATION FOR SEQ ID NO: 133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

TCAAAAAGAG AAGGAAACT TGGTTATTGC TGGGAAAATA GGTCCAGAAC CAGAAATTTT	60
GGCCAATATG TATAAGTTGC TGATTGAAGA AAATACCAGC ATGACTGCGA CTGTTAAACC	120
GAATTTTGGG AAGACAAGCT TCCTTTATGA AGCTCTGAAA AAAGGCGATA TTGACATCTA	180
TCCTGAATTT ACTGGTACGG TGA CTGAAAG TTTGCTTCAA CCATCACCCA AGGTGAGTCA	240
TGAACCAGAA CAGGTTTATC AGGTGGCGCG TGATGGCATT GCTAAGCAGG ATCATCTAGC	300
CTATCTCAA CCCATGTCTT ATCAAACAC CTATGCTGTA GCTGTTCCGA AAAAGATTGC	360
TCAAGAATAT GGCTTGAAGA CCATTTTCTG CTTGAAAAA GTGGAAGGGC AGTTGAAGGC	420
AGGTTTTTACA CTCGAGTTTA ACGACCGTGA AGATGGAAAT AAGGGCTTGC AATCAATGTA	480
TGGTCTCAAT CTCAATGTAG CGACCATTGA GCCAGCCCTT CGCTATCAGG CTATTCAGTC	540
AGGGGATATT CAAATCACGG ATGCCTATTC GACTGATGCG GAATTGGAGC GTTATGATTT	600
ACAGGTCTTG GAAGATGACA AGCAACTCTT CCCACCTTAT CAAGGGGCTC CACTCATGAA	660
AGAAGCTCTT CTCAAGAAAC ACCCAGAGTT GGAAAGAGTT CTTAATACAT TGGCTGGTAA	720
GATTACAGAA AGCCAGATGA GCCAGCTCAA CTACCAAGTC GGTGTTGAAG GCAAGTCAGC	780
AAAGCAAGTA GCCAAGGAGT TTCTCCAAGA ACAAGGTTTG TTGAAGAAA	829

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid

09765272.012201

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Gln Lys Glu Lys Glu Asn Leu Val Ile Ala Gly Lys Ile Gly Pro Glu  
 1 5 10 15  
 Pro Glu Ile Leu Ala Asn Met Tyr Lys Leu Leu Ile Glu Glu Asn Thr  
 20 25 30  
 Ser Met Thr Ala Thr Val Lys Pro Asn Phe Gly Lys Thr Ser Phe Leu  
 35 40 45  
 Tyr Glu Ala Leu Lys Lys Gly Asp Ile Asp Ile Tyr Pro Glu Phe Thr  
 50 55 60  
 Gly Thr Val Thr Glu Ser Leu Leu Gln Pro Ser Pro Lys Val Ser His  
 65 70 75 80  
 Glu Pro Glu Gln Val Tyr Gln Val Ala Arg Asp Gly Ile Ala Lys Gln  
 85 90 95  
 Asp His Leu Ala Tyr Leu Lys Pro Met Ser Tyr Gln Asn Thr Tyr Ala  
 100 105 110  
 Val Ala Val Pro Lys Lys Ile Ala Gln Glu Tyr Gly Leu Lys Thr Ile  
 115 120 125  
 Ser Asp Leu Lys Lys Val Glu Gly Gln Leu Lys Ala Gly Phe Thr Leu  
 130 135 140  
 Glu Phe Asn Asp Arg Glu Asp Gly Asn Lys Gly Leu Gln Ser Met Tyr  
 145 150 155 160  
 Gly Leu Asn Leu Asn Val Ala Thr Ile Glu Pro Ala Leu Arg Tyr Gln  
 165 170 175  
 Ala Ile Gln Ser Gly Asp Ile Gln Ile Thr Asp Ala Tyr Ser Thr Asp  
 180 185 190  
 Ala Glu Leu Glu Arg Tyr Asp Leu Gln Val Leu Glu Asp Asp Lys Gln  
 195 200 205  
 Leu Phe Pro Pro Tyr Gln Gly Ala Pro Leu Met Lys Glu Ala Leu Leu  
 210 215 220  
 Lys Lys His Pro Glu Leu Glu Arg Val Leu Asn Thr Leu Ala Gly Lys  
 225 230 235 240  
 Ile Thr Glu Ser Gln Met Ser Gln Leu Asn Tyr Gln Val Gly Val Glu  
 245 250 255  
 Gly Lys Ser Ala Lys Gln Val Ala Lys Glu Phe Leu Gln Glu Gln Gly  
 260 265 270  
 Leu Leu Lys Lys  
 275

(2) INFORMATION FOR SEQ ID NO: 135:

09765272.012201



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ACGTTCTATT GAGGACCACT TTGATTCAAA CTTCGAATTG GAATATAACC TCAAAGAAAA 60  
 AGGGAAAACA GATCTTTTGA AGCTAGTTGA TAAACAACCT GACATGCGTC TGCATTTTAT 120  
 CCGCCAAACT CATCCACGCG GTCTCGGAGA TGCTGTTTTG CAAGCCAAGG CTTTCGTCGG 180  
 AAATGAACCT TTTGTCGTTA TGCTTGGTGA TGAATTGATG GATATCACAG ACGAAAAGGC 240  
 TGTTCCTACTT ACCAAACAAC TCATGGATGA CTACGAGCGT ACCCAGCGCT CTACTATCGC 300  
 TGTCATGCCA GTCCCTCATG ACGAAGTATC TGCTTACGGG GTTATTGCTC CGCAAGGCCA 360  
 AGGAAAAGAT GGTCTTTACA GTGTTGAAAC CTTTGTGTA AAACCAGCTC CAGAGGACGC 420  
 TCCTAGCGAC CTTGCTATTA TCGGACGCTA CCTCCTCACG CCTGAAATTT TTGAGATTCT 480  
 CGAAAAGCAA GCTCCAGGTG CAGGAAATGA AATTCAGCTG ACAGATGCAA TCGACACCCT 540  
 CAATAAAACA CAACGTGTAT TTGCTCGTGA GTTCAAAGGG GCTCGTTACG ATGTCGGAGA 600  
 CAAGTTTGGC TTCATGAAAA CATCCATCGA CTACGCCCTC AAACACCCAC AAGTCAAAGA 660  
 TGATTTGAAG AATTACCTCA TCCAACCTGG AAAAGAATTG ACTGAGAAGG AA 712

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Arg Ser Ile Glu Asp His Phe Asp Ser Asn Phe Glu Leu Glu Tyr Asn  
 1 5 10 15  
 Leu Lys Glu Lys Gly Lys Thr Asp Leu Leu Lys Leu Val Asp Lys Thr  
 20 25 30  
 Thr Asp Met Arg Leu His Phe Ile Arg Gln Thr His Pro Arg Gly Leu  
 35 40 45  
 Gly Asp Ala Val Leu Gln Ala Lys Ala Phe Val Gly Asn Glu Pro Phe  
 50 55 60  
 Val Val Met Leu Gly Asp Asp Leu Met Asp Ile Thr Asp Glu Lys Ala  
 65 70 75 80

09765272.012201

Val Pro Leu Thr Lys Gln Leu Met Asp Asp Tyr Glu Arg Thr His Ala  
85 90 95

Ser Thr Ile Ala Val Met Pro Val Pro His Asp Glu Val Ser Ala Tyr  
100 105 110

Gly Val Ile Ala Pro Gln Gly Glu Gly Lys Asp Gly Leu Tyr Ser Val  
115 120 125

Glu Thr Phe Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Asp Leu  
130 135 140

Ala Ile Ile Gly Arg Tyr Leu Leu Thr Pro Glu Ile Phe Glu Ile Leu  
145 150 155 160

Glu Lys Gln Ala Pro Gly Ala Gly Asn Glu Ile Gln Leu Thr Asp Ala  
165 170 175

Ile Asp Thr Leu Asn Lys Thr Gln Arg Val Phe Ala Arg Glu Phe Lys  
180 185 190

Gly Ala Arg Tyr Asp Val Gly Asp Lys Phe Gly Phe Met Lys Thr Ser  
195 200 205

Ile Asp Tyr Ala Leu Lys His Pro Gln Val Lys Asp Asp Leu Lys Asn  
210 215 220

Tyr Leu Ile Gln Leu Gly Lys Glu Leu Thr Glu Lys Glu  
225 230 235

## (2) INFORMATION FOR SEQ ID NO: 137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CGCTCAAAAT ACCAGAGGTG TTCAGCTAAT CGAGCACGTT TCTCCTCAAA TGTTGAAAGC 60

CCAATTGGAG AGTGTCTTTT CTGATATTCC ACCTCAGGCT GTAAAACTG GAATGTTGGC 120

TACTACTGAA ATCATGGAAA TCATCCAACC CTATCTTAAA AACTGGATT GTCCCTATGT 180

CCTTGATCCT GTTATGGTTG CTACAAGTGG AGATGCCTTG ATTGACTCAA ATGCTAGAGA 240

CTATCTCAAA ACAAACCTAC TACCTCTAGC AACTATTATT ACGCCAAATC TTCCTGAAGC 300

AGAAGAGATT GTTGGTTTTT CAATCCATGA CCCCAGAGAC ATGCAGCGTG CTGGTCGCCT 360

GATTTTAAAA GAATTTGGTC CTCAGTCTGT GGTTATCAAA GGCGGACATC TCAAAGGTGG 420

TGCTAAAGAT TTCCTCTTTA CCAAGAATGA ACAATTTGTC TGGGAAAGCC CACGAATTCA 480

AACCTGTCAC ACCCATGGTA CT 502

## (2) INFORMATION FOR SEQ ID NO:138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ala	Gln	Asn	Thr	Arg	Gly	Val	Gln	Leu	Ile	Glu	His	Val	Ser	Pro	Gln	1	5	10	15
Met	Leu	Lys	Ala	Gln	Leu	Glu	Ser	Val	Phe	Ser	Asp	Ile	Pro	Pro	Gln	20	25	30	
Ala	Val	Lys	Thr	Gly	Met	Leu	Ala	Thr	Thr	Glu	Ile	Met	Glu	Ile	Ile	35	40	45	
Gln	Pro	Tyr	Leu	Lys	Lys	Leu	Asp	Cys	Pro	Tyr	Val	Leu	Asp	Pro	Val	50	55	60	
Met	Val	Ala	Thr	Ser	Gly	Asp	Ala	Leu	Ile	Asp	Ser	Asn	Ala	Arg	Asp	65	70	75	80
Tyr	Leu	Lys	Thr	Asn	Leu	Leu	Pro	Leu	Ala	Thr	Ile	Ile	Thr	Pro	Asn	85	90	95	
Leu	Pro	Glu	Ala	Glu	Glu	Ile	Val	Gly	Phe	Ser	Ile	His	Asp	Pro	Glu	100	105	110	
Asp	Met	Gln	Arg	Ala	Gly	Arg	Leu	Ile	Leu	Lys	Glu	Phe	Gly	Pro	Gln	115	120	125	
Ser	Val	Val	Ile	Lys	Gly	Gly	His	Leu	Lys	Gly	Gly	Ala	Lys	Asp	Phe	130	135	140	
Leu	Phe	Thr	Lys	Asn	Glu	Gln	Phe	Val	Trp	Glu	Ser	Pro	Arg	Ile	Gln	145	150	155	160
Thr	Cys	His	Thr	His	Gly	Thr	165												

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

AATTGTACAA	TTAGAAAAAG	ATAGCAAATC	AGACAAAGAA	CAAGTTGATA	AACTATTTGA	60
ATCATTTGAT	GCATCTTCAG	ATGAATCTAT	TTCTAAATTA	AAAGAACTAT	CTGAAACTTC	120
ACTTAAACC	GATGCAGGTA	AAGACTATCT	TAATAACAAA	GTCAAAGAAT	CATCTAAAGC	180
AATTGTAGAT	TTTCATTTGC	AAAAAGGTTT	GGCTTATGAT	GTAAAGATT	CAGATGACAA	240

ATTTAAAGAT AAAGCAACTC TTGAAACAAA TGTAAGAA ATTACAAAAC AAATTGATTT 300  
 TATCAAAAAA GTTGATGAAA CTTTTAAACA AGAGAATTTG GAAGAACTC TTAAATCTCT 360  
 AAATGATCTT GTTGATAAAT ATCAAAAACA AATCGAACTT TTGAAGAAAG AAGAAGAAAA 420  
 AGCTGCTGAA AAAGCTGCTG AAAAAGCAAA GGAATCTTCT AGTCAAAGTA ATTCTTCTGG 480  
 TAGTGCTTCT AATGAGTCTT ATAATGGATC TTCCAATTCA AATGTAGATT ATAGTTCATC 540  
 TGAACAAACT AATGGATATT CAAATAATTA TGGCGGTCAA GATTATTCTG GTTCAGGAGA 600  
 TAGTTCAACA AATGGTGGAT CATCAGAACA ATATTCATCT AGCAATTCAA ACAGCGGAGC 660  
 AAATAATGTC TACAGATATA AAGGCACTGG TGCTGACGGC TATCAAAGAT ACTACTACAA 720  
 AGATCATAAT AATGGAGATG TGTATGATGA CGATGGAAAT TACCTTGGGA ACTTTGGTGG 780  
 CGGCATTGCA GAACCTAGTC AACGC 805

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ile	Val	Gln	Leu	Glu	Lys	Asp	Ser	Lys	Ser	Asp	Lys	Glu	Gln	Val	Asp	1	5	10	15
Lys	Leu	Phe	Glu	Ser	Phe	Asp	Ala	Ser	Ser	Asp	Glu	Ser	Ile	Ser	Lys	20	25	30	
Leu	Lys	Glu	Leu	Ser	Glu	Thr	Ser	Leu	Lys	Thr	Asp	Ala	Gly	Lys	Asp	35	40	45	
Tyr	Leu	Asn	Asn	Lys	Val	Lys	Glu	Ser	Ser	Lys	Ala	Ile	Val	Asp	Phe	50	55	60	
His	Leu	Gln	Lys	Gly	Leu	Ala	Tyr	Asp	Val	Lys	Asp	Ser	Asp	Asp	Lys	65	70	75	80
Phe	Lys	Asp	Lys	Ala	Thr	Leu	Glu	Thr	Asn	Val	Lys	Glu	Ile	Thr	Lys	85	90	95	
Gln	Ile	Asp	Phe	Ile	Lys	Lys	Val	Asp	Glu	Thr	Phe	Lys	Gln	Glu	Asn	100	105	110	
Leu	Glu	Glu	Thr	Leu	Lys	Ser	Leu	Asn	Asp	Leu	Val	Asp	Lys	Tyr	Gln	115	120	125	
Lys	Gln	Ile	Glu	Leu	Leu	Lys	Lys	Glu	Glu	Glu	Lys	Ala	Ala	Glu	Lys	130	135	140	
Ala	Ala	Glu	Lys	Ala	Lys	Glu	Ser	Ser	Ser	Gln	Ser	Asn	Ser	Ser	Gly	145	150	155	160

09765272-012201

254

Ser Ala Ser Asn Glu Ser Tyr Asn Gly Ser Ser Asn Ser Asn Val Asp  
 165 170 175  
 Tyr Ser Ser Ser Glu Gln Thr Asn Gly Tyr Ser Asn Asn Tyr Gly Gly  
 180 185 190  
 Gln Asp Tyr Ser Gly Ser Gly Asp Ser Ser Thr Asn Gly Gly Ser Ser  
 195 200 205  
 Glu Gln Tyr Ser Ser Ser Asn Ser Asn Ser Gly Ala Asn Asn Val Tyr  
 210 215 220  
 Arg Tyr Lys Gly Thr Gly Ala Asp Gly Tyr Gln Arg Tyr Tyr Tyr Lys  
 225 230 235 240  
 Asp His Asn Asn Gly Asp Val Tyr Asp Asp Asp Gly Asn Tyr Leu Gly  
 245 250 255  
 Asn Phe Gly Gly Gly Ile Ala Glu Pro Ser Gln Arg  
 260 265

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TCTGACCAAG CAAAAAGAAG CAGTCAATGA CAAAGGAAAA GCAGCTGTTG TTAAGGTGGT	60
GGAAAGCCAG GCAGAACTTT ATAGCTTAGA AAAGAATGAA GATGCTAGCC TAAGAAAAGTT	120
ACAAGCAGAT GGACGCATCA CGGAAGAACA GGCTAAAGCT TATAAAGAAT ACAATGATAA	180
AAATGGAGGA GCAAATCGTA AAGTCAATGA T	211

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu Thr Lys Gln Lys Glu Ala Val Asn Asp Lys Gly Lys Ala Ala Val  
 1 5 10 15  
 Val Lys Val Val Glu Ser Gln Ala Glu Leu Tyr Ser Leu Glu Lys Asn  
 20 25 30  
 Glu Asp Ala Ser Leu Arg Lys Leu Gln Ala Asp Gly Arg Ile Thr Glu  
 35 40 45

09765272.012201

Glu Gln Ala Lys Ala Tyr Lys Glu Tyr Asn Asp Lys Asn Gly Gly Ala  
50 55 60

Asn Arg Lys Val Asn Asp  
65 70

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC GGTAGAGGAA CAGATTTTCT TTATGGAGTT	60
TGAAGAACTC TATCGGGAAA CCCAAAAACG CAGTGTAGCC AGTCAGCAAA AGACTAGTCT	120
GAACCTAGAT GGGCAGACGC TTAGCAATGG CAGTCAAAAG TTGCCAGTCC CTAAAGGAAT	180
TCAGGCCCCA TCAGGCCAAA GTATTACATT TGACCGAGCT GGGGGCAATT CGTCCCTGGC	240
TAAGGTTGAA TTTAGACCA GTAAAGGAGC GATTGCTAT CAATTATATC TAGGAAATGG	300
AAAAATTAAA CGCATTAAGG AAACAAAAAA T	331

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 110 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Ser Gly Ser Val Gln Ser Thr Phe Ser Ala Val Glu Glu Gln Ile Phe	1	5	10	15
Phe Met Glu Phe Glu Glu Leu Tyr Arg Glu Thr Gln Lys Arg Ser Val	20	25	30	
Ala Ser Gln Gln Lys Thr Ser Leu Asn Leu Asp Gly Gln Thr Leu Ser	35	40	45	
Asn Gly Ser Gln Lys Leu Pro Val Pro Lys Gly Ile Gln Ala Pro Ser	50	55	60	
Gly Gln Ser Ile Thr Phe Asp Arg Ala Gly Gly Asn Ser Ser Leu Ala	65	70	75	80
Lys Val Glu Phe Gln Thr Ser Lys Gly Ala Ile Arg Tyr Gln Leu Tyr	85	90	95	
Leu Gly Asn Gly Lys Ile Lys Arg Ile Lys Glu Thr Lys Asn	100	105	110	

09765272.012204

## (2) INFORMATION FOR SEQ ID NO: 145:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

GGGACAAATT CAAAAAATA GGCAAGAGGA AGCAAAAATC TTGCAAAAGG AAGAAGTCTT 60  
 GAGGGTAGCT AAGATGGCCC TGCAGACGGG GCAAAATCAG GTAAGCATCA ACGGAGTTGA 120  
 GATTCAGGTA TTTTCTAGTG AAAAAGGATT GGAGGTCTAC CATGGTTCAG AACAGTTGTT 180  
 GGCAATCAAA GAGCCA 196

## (2) INFORMATION FOR SEQ ID NO:146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Gly Gln Ile Gln Lys Asn Arg Gln Glu Glu Ala Lys Ile Leu Gln Lys  
 1 5 10 15  
 Glu Glu Val Leu Arg Val Ala Lys Met Ala Leu Gln Thr Gly Gln Asn  
 20 25 30  
 Gln Val Ser Ile Asn Gly Val Glu Ile Gln Val Phe Ser Ser Glu Lys  
 35 40 45  
 Gly Leu Glu Val Tyr His Gly Ser Glu Gln Leu Leu Ala Ile Lys Glu  
 50 55 60  
 Pro  
 65

## (2) INFORMATION FOR SEQ ID NO: 147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:-----

TCGCTACCAG CAACAAAGCG AGCAAAAGGA GTGGCTCTTG TTTGTGGACC AACTTGAGGT 60

0976522.012201

AGAATTAGAC CGTTCGCAGT TCGAAAAAGT AGAAGGCAAT CGCCTATACA TGAAGCAAGA 120  
 TGGCAAGGAC ATCGCCATCG GTAAGTCAAA GTCAGATGAT TTCCGTAAAA CGAATGCTCG 180  
 TGGTCGAGGT TATCAGCCTA TGGTTTATGG ACTCAAATCT GTACGGATTA CAGAGGACAA 240  
 TCAACTGGTT CGCTTTCATT TCCAGTTCCA AAAAGGCTTA GAAAGGGAGT TCATCTATCG 300  
 TGTGGAAAAA GAAAAAAGT 319

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Arg Tyr Gln Gln Gln Ser Glu Gln Lys Glu Trp Leu Leu Phe Val Asp  
 1 5 10 15  
 Gln Leu Glu Val Glu Leu Asp Arg Ser Gln Phe Glu Lys Val Glu Gly  
 20 25 30  
 Asn Arg Leu Tyr Met Lys Gln Asp Gly Lys Asp Ile Ala Ile Gly Lys  
 35 40 45  
 Ser Lys Ser Asp Asp Phe Arg Lys Thr Asn Ala Arg Gly Arg Gly Tyr  
 50 55 60  
 Gln Pro Met Val Tyr Gly Leu Lys Ser Val Arg Ile Thr Glu Asp Asn  
 65 70 75 80  
 Gln Leu Val Arg Phe His Phe Gln Phe Gln Lys Gly Leu Glu Arg Glu  
 85 90 95  
 Phe Ile Tyr Arg Val Glu Lys Glu Lys Ser  
 100 105

## (2) INFORMATION FOR SEQ ID NO: 149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

GAACCGACAA GTCGCCCACT ATCAAGACTA TGCTTTGAAT AAAGAAAAAT TGGTTGCTTT 60  
 TGCTATGGCT AAACGAACCA AAGATAAGGT TGAGCAAGAA AGTGGGGAAC AGTTTTTTAA 120  
 TCTAGGTCAG GTAAGCTATC AAAACAAGAA AACTGGCTTA GTGACGAGGG TTCGTACGGA 180  
 TAAGAGCCAA TATGAGTTTC TGTTTCCTTC AGTCAAAATC AAAGAAGAGA AAAGAGATAA 240

09765272.012204



AAAGGAAGAG GTAGCGACCG ATTCAAGCGA AAAAGTGGAG AAGAAAAAAT CAGAAGAGAA 300  
GCCTGAAAAG AAAGAGAATT CA 322

## (2) INFORMATION FOR SEQ ID NO:150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Asn Arg Gln Val Ala His Tyr Gln Asp Tyr Ala Leu Asn Lys Glu Lys  
1 5 10 15

Leu Val Ala Phe Ala Met Ala Lys Arg Thr Lys Asp Lys Val Glu Gln  
20 25 30

Glu Ser Gly Glu Gln Phe Phe Asn Leu Gly Gln Val Ser Tyr Gln Asn  
35 40 45

Lys Lys Thr Gly Leu Val Thr Arg Val Arg Thr Asp Lys Ser Gln Tyr  
50 55 60

Glu Phe Leu Phe Pro Ser Val Lys Ile Lys Glu Lys Arg Asp Lys  
65 70 75 80

Lys Glu Glu Val Ala Thr Asp Ser Ser Glu Lys Val Glu Lys Lys Lys  
85 90 95

Ser Glu Glu Lys Pro Glu Lys Lys Glu Asn Ser  
100 105

## (2) INFORMATION FOR SEQ ID NO: 151:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

GGTTGTCGGC TGGCAATATA TCCCGTTTCC ATCTAAAGGT AGTACAATTG GTCCTTACCC 60  
AAATGGTATC AGATTAGAAG GTTTTCCAAA GTCAGAGTGG TACTACTTCG ATAAAAATGG 120  
AGTGCTACAA GAGTTTGTGG GTTGGAAAAC ATTAGAGATT AAAACTAAAG ACAGTGTTGG 180  
AAGAAAGTAC GGGGAAAAAC GTGAAGATTC AGAAGATAAA GAAGAGAAGC GTTATTATAC 240  
GAATATTAC TTTAATCAAA ATCATTCTTT AGAGACAGGT TGGCTTTATG ATCAGTCTAA 300  
CTGGTATTAT CTAGCTAAGA CGGAAATTAA TGGAGAAAAC TACCTTGGTG GTGAAAGACG 360

09765272.012201

TGCGGGGTGG ATAAACGATG ATTCGACTTG GTACTACCTA GATCCAACAA CTGGTATTAT 420  
 GCAAACAGGT TGGCAATATC TAGGTAATAA GTGGTACTAC CTCCGTTCTT CAGGAGCAAT 480  
 GGCCACTGGC TGGTATCAGG AAGGTACCAC TTGGTATTAT TTAGACCACC CAAATGGCGA 540  
 TATGAAAACA GGTTGGCAAA ACCTTGGGAA CAAATGGTAC TATCTCCGTT CATCAGGAGC 600  
 TATGGCAACT GGTTGGTATC AAGATGGTTC AACTTGGTAC TACCTAAATG CAGGTAATGG 660  
 AGACATGAAG ACAGGTTGGT TCCAGGTCAA TGGCAACTGG TACTATGCTT ATAGCTCAGG 720  
 TGCTTTGGCA GTGAATACGA CCGTAGATGG CTATTCTGTC AACTATAATG GCGAATGGGT 780  
 TCGG 784

## (2) INFORMATION FOR SEQ ID NO:152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Val Val Gly Trp Gln Tyr Ile Pro Phe Pro Ser Lys Gly Ser Thr Ile  
 1 5 10 15  
 Gly Pro Tyr Pro Asn Gly Ile Arg Leu Glu Gly Phe Pro Lys Ser Glu  
 20 25 30  
 Trp Tyr Tyr Phe Asp Lys Asn Gly Val Leu Gln Glu Phe Val Gly Trp  
 35 40 45  
 Lys Thr Leu Glu Ile Lys Thr Lys Asp Ser Val Gly Arg Lys Tyr Gly  
 50 55 60  
 Glu Lys Arg Glu Asp Ser Glu Asp Lys Glu Glu Lys Arg Tyr Tyr Thr  
 65 70 75 80  
 Asn Tyr Tyr Phe Asn Gln Asn His Ser Leu Glu Thr Gly Trp Leu Tyr  
 85 90 95  
 Asp Gln Ser Asn Trp Tyr Tyr Leu Ala Lys Thr Glu Ile Asn Gly Glu  
 100 105 110  
 Asn Tyr Leu Gly Gly Glu Arg Arg Ala Gly Trp Ile Asn Asp Asp Ser  
 115 120 125  
 Thr Trp Tyr Tyr Leu Asp Pro Thr Thr Gly Ile Met Gln Thr Gly Trp  
 130 135 140  
 Gln Tyr Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met  
 145 150 155 160  
 Ala Thr Gly Trp Tyr Gln Glu Gly Thr Thr Trp Tyr Tyr Leu Asp His  
 165 170 175  
 Pro Asn Gly Asp Met Lys Thr Gly Trp Gln Asn Leu Gly Asn Lys Trp

09765272.012201

09765272.012204

260

180	185	190
Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp 195 200 205		
Gly Ser Thr Trp Tyr Tyr Leu Asn Ala Gly Asn Gly Asp Met Lys Thr 210 215 220		
Gly Trp Phe Gln Val Asn Gly Asn Trp Tyr Tyr Ala Tyr Ser Ser Gly 225 230 235 240		
Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Ser Val Asn Tyr Asn 245 250 255		
Gly Glu Trp Val Arg 260		

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GGCCAAATCA GAATGGGTAG AAGACAAGGG AGCCTTTTAT TATCTTGACC AAGATGGAAA	60
GATGAAAAGA AATGCTTGGG TAGGAACTTC CTATGTTGGT GCAACAGGTG CCAAAGTAAT	120
AGAAGACTGG GTCTATGATT CTCAATACGA TGCTTGTTTT TATATCAAAG CAGATGGACA	180
GCACGCAGAG AAAGAATGGC TCCAAATTAA AGGGAAGGAC TATTATTTCA AATCCGGTGG	240
TTATCTACTG ACAAGTCAGT GGATTAATCA AGCTTATGTG AATGCTAGTG GTGCCAAAGT	300
ACAGCAAGGT TGGCTTTTTG ACAAACAATA CCAATCTTGG TTTTACATCA AAGAAAATGG	360
AAACTATGCT GATAAAGAAT GGATTTTCGA GAATGGTCAC TATTATTATC TAAATCCGG	420
TGGCTACATG GCAGCCAATG AATGGATTGG GGATAAGGAA TCTTGGTTTT ATCTCAAATT	480
TGATGGGAAA ATGGCTGAAA AAGAATGGGT CTACGATTCT CATAGTCAAG CTTGGTACTA	540
CTTCAAATCC GGTGGTTACA TGACAGCCAA TGAATGGATT TGGGATAAGG AATCTTGTTT	600
TTATCTCAA TCTGATGGGA AAATAGCTGA AAAAGAATGG GTCTACGATT CTCATAGTCA	660
AGCTTGGTAC TACTTCAAAT CCGGTGGTTA CATGACAGCC AATGAATGGA TTTGGGATAA	720
GGAATCTTGG TTTTACCTCA AATCTGATGG GAAAATAGCT GAAAAAGAAT GGGTCTACGA	780
TTCTCATAGT CAAGCTTGGT ACTACTTCAA ATCTGGTGGC TACATGGCGA AAAATGAGAC	840
AGTAGATGGT TATCAGCTTG GAAGCGATGG TAAATGGCTT GGAGGAAAAA CTACAAATGA	900
AAATGCTGCT TACTATCAAG TAGTGCCTGT TACAGCCAAT GTTTATGATT CAGATGGTGA	960
AAAGCTTTCC TATATATCGC AAGGTAGTGT CGTATGGCTA GATAAGGATA GAAAAAGTGA	1020

TGACAAGCGC TTGGCTATTA CTATTTCTGG TTTGTCAGGC TATATGAAAA CAGAAGATTT 1080  
 ACAAGCGCTA GATGCTAGTA AGGACTTTAT CCCTTATTAT GAGAGTGATG GCCACCGTTT 1140  
 TTATCACTAT GTGGCTCAGA ATGCTAGTAT CCCAGTAGCT TCTCATCTTT CTGATATGGA 1200  
 AGTAGGCAAG AAATATTATT CGGCAGATGG CCTGCATTTT GATGGTTTTA AGCTTGAGAA 1260  
 TCCCTTCCTT TTCAAAGATT TAACAGAGGC TACAAACTAC AGTGCTGAAG AATTGGATAA 1320  
 GGTATTTAGT TTGCTAAACA TTAACAATAG CCTTTTGGAG AACAAGGGCG CTACTIONTTAA 1380  
 GGAAGCCGAA GAACATTACC ATATCAATGC TCTTTATCTC CTTGCCCCATA GTGCCCTAGA 1440  
 AAGTAACTGG GGAAGAAGTA AAATTGCCAA AGATAAGAAT AATTTCTTTG GCATTACAGC 1500  
 CTATGATACG ACCCCTTACC TTTCTGCTAA GACATTTGAT GATGTGGATA AGGGAATTTT 1560  
 AGGTGCAACC AAGTGGATTA AGGAAAATTA TATCGATAGG GGAAGAACTT TCCTTGAAAA 1620  
 CAAGGCTTCT GGTATGAATG TGGAATATGC TTCAGACCCT TATTGGGGCG AAAAAATTGC 1680  
 TAGTGTGATG ATGAAAATCA ATGAGAAG 1708

## (2) INFORMATION FOR SEQ ID NO:154:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Ala Lys Ser Glu Trp Val Glu Asp Lys Gly Ala Phe Tyr Tyr Leu Asp  
 1 5 10 15  
 Gln Asp Gly Lys Met Lys Arg Asn Ala Trp Val Gly Thr Ser Tyr Val  
 20 25 30  
 Gly Ala Thr Gly Ala Lys Val Ile Glu Asp Trp Val Tyr Asp Ser Gln  
 35 40 45  
 Tyr Asp Ala Trp Phe Tyr Ile Lys Ala Asp Gly Gln His Ala Glu Lys  
 50 55 60  
 Glu Trp Leu Gln Ile Lys Gly Lys Asp Tyr Tyr Phe Lys Ser Gly Gly  
 65 70 75 80  
 Tyr Leu Leu Thr Ser Gln Trp Ile Asn Gln Ala Tyr Val Asn Ala Ser  
 85 90 95  
 Gly Ala Lys Val Gln Gln Gly Trp Leu Phe Asp Lys Gln Tyr Gln Ser  
 100 105 110  
 Trp Phe Tyr Ile Lys Glu Asn Gly Asn Tyr Ala Asp Lys Glu Trp Ile  
 115 120 125  
 Phe Glu Asn Gly His Tyr Tyr Tyr Leu Lys Ser Gly Gly Tyr Met Ala  
 130 135 140

09765272.012201

Ala Asn Glu Trp Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Phe  
 145 150 155 160  
 Asp Gly Lys Met Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln  
 165 170 175  
 Ala Trp Tyr Tyr Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp  
 180 185 190  
 Ile Trp Asp Lys Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile  
 195 200 205  
 Ala Glu Lys Glu Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr  
 210 215 220  
 Phe Lys Ser Gly Gly Tyr Met Thr Ala Asn Glu Trp Ile Trp Asp Lys  
 225 230 235 240  
 Glu Ser Trp Phe Tyr Leu Lys Ser Asp Gly Lys Ile Ala Glu Lys Glu  
 245 250 255  
 Trp Val Tyr Asp Ser His Ser Gln Ala Trp Tyr Tyr Phe Lys Ser Gly  
 260 265 270  
 Gly Tyr Met Ala Lys Asn Glu Thr Val Asp Gly Tyr Gln Leu Gly Ser  
 275 280 285  
 Asp Gly Lys Trp Leu Gly Gly Lys Thr Thr Asn Glu Asn Ala Ala Tyr  
 290 295 300  
 Tyr Gln Val Val Pro Val Thr Ala Asn Val Tyr Asp Ser Asp Gly Glu  
 305 310 315 320  
 Lys Leu Ser Tyr Ile Ser Gln Gly Ser Val Val Trp Leu Asp Lys Asp  
 325 330 335  
 Arg Lys Ser Asp Asp Lys Arg Leu Ala Ile Thr Ile Ser Gly Leu Ser  
 340 345 350  
 Gly Tyr Met Lys Thr Glu Asp Leu Gln Ala Leu Asp Ala Ser Lys Asp  
 355 360 365  
 Phe Ile Pro Tyr Tyr Glu Ser Asp Gly His Arg Phe Tyr His Tyr Val  
 370 375 380  
 Ala Gln Asn Ala Ser Ile Pro Val Ala Ser His Leu Ser Asp Met Glu  
 385 390 395 400  
 Val Gly Lys Lys Tyr Tyr Ser Ala Asp Gly Leu His Phe Asp Gly Phe  
 405 410 415  
 Lys Leu Glu Asn Pro Phe Leu Phe Lys Asp Leu Thr Glu Ala Thr Asn  
 420 425 430  
 Tyr Ser Ala Glu Glu Leu Asp Lys Val Phe Ser Leu Leu Asn Ile Asn  
 435 440 445  
 Asn Ser Leu Leu Glu Asn Lys Gly Ala Thr Phe Lys Glu Ala Glu Glu  
 450 455 460  
 His Tyr His Ile Asn Ala Leu Tyr Leu Leu Ala His Ser Ala Leu Glu  
 465 470 475 480

09765272-012201

(2) INFORMATION FOR SEQ ID NO: 155:

(A) LENGTH: 946 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

ATTTCGAGAT	GATTCTGAAG	GATGGCAGTT	TGTCCAAGAA	AATGGTAGAA	CCTACTACAA	60
AAAGGGGGAT	CTAAAAGAAA	CCTACTGGAG	AGTGATAGAT	GGGAAGTACT	ATTATTTTGA	120
TCCTTTATCC	GGAGAGATGG	TTGTCGGCTG	GCAATATATA	CCTGCTCCAC	ACAAGGGGGT	180
TACGATTGGT	CCTTCTCCAA	GAATAGAGAT	TGCTCTTAGA	CCAGATTGGT	TTTATTTTGG	240
TCAAGATGGT	GTATTACAAG	AATTTGTTGG	CAAGCAAGTT	TTAGAAGCAA	AAACTGCTAC	300
GAATACCAAC	AAACATCATG	GGGAAGAATA	TGATAGCCAA	GCAGAGAAAC	GAGTCTATTA	360
TTTTGAAGAT	CAGCGTAGTT	ATCATACTTT	AAAAACTGGT	TGGATTTATG	AAGAGGGTCA	420
TTGGTATTAT	TTACAGAAGG	ATGGTGGCTT	TGATTGCGCG	ATCAACAGAT	TGACGGTTGG	480
AGAGCTAGCA	CGTGGTTGGG	TTAAGGATTA	CCCTCTTACG	TATGATGAAG	AGAAGCTAAA	540
AGCAGCTCCA	TGGTACTATC	TAAATCCAGC	AACTGGCATT	ATGCAAACAG	GTTGGCAATA	600
TCTAGGTAAT	AGATGGTACT	ACCTCCATTC	GTCAGGAGCT	ATGGCAACTG	GCTGGTATAA	660
GGAAGGCTCA	ACTTGGTACT	ATCTAGATGC	TGAAAATGGT	GATATGAGAA	CTGGCTGGCA	720
AAACCTTGGG	AACAAATGGT	ACTATCTCCG	TTCATCAGGA	GCTATGGCAA	CTGGTTGGTA	780
TCAGGAAAGT	TCGACTTGGT	ACTATCTAAA	TGCAAGTAAT	GGAGATATGA	AAACAGGCTG	840
GTTCCAAGTC	AATGGTAACT	GGTACTATGC	CTATGATTCA	GGTGCTTTAG	CTGTTAATAC	900
CACAGTAGGT	GGTTACTACT	TAAACTATAA	TGGTGAATGG	GTTAAG		946

## (2) INFORMATION FOR SEQ ID NO:156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

Val Phe Ala Asp Asp Ser Glu Gly Trp Gln Phe Val Gln Glu Asn Gly
1           5           10           15

Arg Thr Tyr Tyr Lys Lys Gly Asp Leu Lys Glu Thr Tyr Trp Arg Val
          20           25           30

Ile Asp Gly Lys Tyr Tyr Tyr Phe Asp Pro Leu Ser Gly Glu Met Val
          35           40           45

Val Gly Trp Gln Tyr Ile Pro Ala Pro His Lys Gly Val Thr Ile Gly
          50           55           60

Pro Ser Pro Arg Ile Glu Ile Ala Leu Arg Pro Asp Trp Phe Tyr Phe
65           70           75           80

Gly Gln Asp Gly Val Leu Gln Glu Phe Val Gly Lys Gln Val Leu Glu
          85           90           95

Ala Lys Thr Ala Thr Asn Thr Asn Lys His His Gly Glu Glu Tyr Asp
          100          105          110

Ser Gln Ala Glu Lys Arg Val Tyr Tyr Phe Glu Asp Gln Arg Ser Tyr
          115          120          125

His Thr Leu Lys Thr Gly Trp Ile Tyr Glu Glu Gly His Trp Tyr Tyr
          130          135          140

Leu Gln Lys Asp Gly Gly Phe Asp Ser Arg Ile Asn Arg Leu Thr Val
145          150          155          160

Gly Glu Leu Ala Arg Gly Trp Val Lys Asp Tyr Pro Leu Thr Tyr Asp
          165          170          175

Glu Glu Lys Leu Lys Ala Ala Pro Trp Tyr Tyr Leu Asn Pro Ala Thr
          180          185          190

Gly Ile Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Arg Trp Tyr Tyr
          195          200          205

Leu His Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Lys Glu Gly Ser
          210          215          220

Thr Trp Tyr Tyr Leu Asp Ala Glu Asn Gly Asp Met Arg Thr Gly Trp
225          230          235          240

Gln Asn Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met
          245          250          255

Ala Thr Gly Trp Tyr Gln Glu Ser Ser Thr Trp Tyr Tyr Leu Asn Ala
          260          265          270

```

00765072.012204

Ser Asn Gly Asp Met Lys Thr Gly Trp Phe Gln Val Asn Gly Asn Trp  
 275 280 285

Tyr Tyr Ala Tyr Asp Ser Gly Ala Leu Ala Val Asn Thr Thr Val Gly  
 290 295 300

Gly Tyr Tyr Leu Asn Tyr Asn Gly Glu Trp Val Lys  
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGTCGCTGCA AATGAACTG AAGTAGCAAA AACTTCGCAG GATACAACGA CAGCTTCAAG	60
TAGTTCAGAG CAAAATCAGT CTTCTAATAA AACGCAAACG AGCGCAGAAG TACAGACTAA	120
TGCTGCTGCC CACTGGGATG GGGATTATTA TGTAAGGAT GATGGTTCTA AAGCTCAAAG	180
TGAATGGATT TTTGACAAC ACTATAAGGC TTGGTTTTAT ATTAATTCAG ATGGTCGTTA	240
CTCGCAGAAT GAATGGCATG GAAATTACTA CCTGAAATCA GGTGGATATA TGGCCCCAAA	300
CGAGTGGATC TATGACAGTA ATTACAAGAG TTGGTTTTAT CTCAAGTCAG ATGGGGCTTA	360
TGCTCATCAA GAATGGCAAT TGATTGGAAG TAAGTGGTAC TACTTCAAGA AGTGGGGTTA	420
CATGGCTAAA AGCCAATGGC AAGGAAGTTA TTTCTTGAAT GGTCAAGGAG CTATGATGCA	480
AAATGAATGG CTSCTATGAT CCAGCCTATT CTGCTTATTT TTATCTAAAA TCCGATGGAA	540
CTTATGCTAA CCAAGAGTGG CAAAAAGTGG GCGGCAAATG GTACTATTTT AAGAAGTGGG	600
GCTATATGGC TCGGAATGAG TGGCAAGGCA ACTACTATTT GACTGGAAGT GGTGCCATGG	660
CGACTGACGA AGTGATTATG GATGGTACTC GCTATATCTT TCGGCCTCT GGTGAGCTCA	720
AAGAAAAAAA AGATTTGAAT GTCGGCTGGG TTCACAGAGA TGGTAAGCGC TATTTCTTTA	780
ATAATAGAGA AGAACAAGTG GGAACCGAAC ATGCTAAGAA AGTCATTGAT ATTAGTGAGC	840
ACAATGGTCG TATCAATGAT TGGAAAAAGG TTATTGATGA GAACGAAGTG GATGGTGTCA	900
TTGTTTCGTCT AGGTTATAGC GGTAAAGAAG ACAAGGAATT GGCGCATAAC ATTAAGGAGT	960
TAAACCGTCT GGGAATTCCT TATGGTGTCT ATCTCTATAC CTATGCTGAA AATGAGACCG	1020
ATGCTGAGAG TGACGCTAAA CAGACCATTG AACTTATAAA GAAATACAAT ATGAACCTGT	1080
CTTACCCTAT CTATTATGAT GTTGAGAATT GGAATATGT AAATAAGAGC AAGAGAGCTC	1140
CAAGTGATAC AGGCACTTGG GTTAAAATCA TCAACAAGTA CATGGACACG ATGAAGCAGG	1200
CGGGTTATCA AAATGTGTAT GTCTATAGCT ATCGTAGTTT ATTACAGACG CGTTTAAAC	1260

09765272.012201



ACCCAGATAT TTAAAAACAT GTAAACTGGG TAGCGGCCTA TACGAATGCT TTAGAATGGG 1320  
 AAAACCCTCA TTATTCAGGA AAAAAAGGTT GGCAATATAC CTCTTCTGAA TACATGAAAG 1380  
 GAATCCAAGG GCGCGTAGAT GTCAGCGTTT GGTAT 1415

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Val	Ala	Ala	Asn	Glu	Thr	Glu	Val	Ala	Lys	Thr	Ser	Gln	Asp	Thr	Thr	1	5	10	15
Thr	Ala	Ser	Ser	Ser	Ser	Glu	Gln	Asn	Gln	Ser	Ser	Asn	Lys	Thr	Gln	20	25	30	
Thr	Ser	Ala	Glu	Val	Gln	Thr	Asn	Ala	Ala	Ala	His	Trp	Asp	Gly	Asp	35	40	45	
Tyr	Tyr	Val	Lys	Asp	Asp	Gly	Ser	Lys	Ala	Gln	Ser	Glu	Trp	Ile	Phe	50	55	60	
Asp	Asn	Tyr	Tyr	Lys	Ala	Trp	Phe	Tyr	Ile	Asn	Ser	Asp	Gly	Arg	Tyr	65	70	75	80
Ser	Gln	Asn	Glu	Trp	His	Gly	Asn	Tyr	Tyr	Leu	Lys	Ser	Gly	Gly	Tyr	85	90	95	
Met	Ala	Gln	Asn	Glu	Trp	Ile	Tyr	Asp	Ser	Asn	Tyr	Lys	Ser	Trp	Phe	100	105	110	
Tyr	Leu	Lys	Ser	Asp	Gly	Ala	Tyr	Ala	His	Gln	Glu	Trp	Gln	Leu	Ile	115	120	125	
Gly	Asn	Lys	Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Lys	Ser	130	135	140	
Gln	Trp	Gln	Gly	Ser	Tyr	Phe	Leu	Asn	Gly	Gln	Gly	Ala	Met	Met	Gln	145	150	155	160
Asn	Glu	Trp	Leu	Tyr	Asp	Pro	Ala	Tyr	Ser	Ala	Tyr	Phe	Tyr	Leu	Lys	165	170	175	
Ser	Asp	Gly	Thr	Tyr	Ala	Asn	Gln	Glu	Trp	Gln	Lys	Val	Gly	Gly	Lys	180	185	190	
Trp	Tyr	Tyr	Phe	Lys	Lys	Trp	Gly	Tyr	Met	Ala	Arg	Asn	Glu	Trp	Gln	195	200	205	
Gly	Asn	Tyr	Tyr	Leu	Thr	Gly	Ser	Gly	Ala	Met	Ala	Thr	Asp	Glu	Val	210	215	220	
Ile	Met	Asp	Gly	Thr	Arg	Tyr	Ile	Phe	Ala	Ala	Ser	Gly	Glu	Leu	Lys				

00765272.0122001

225		230		235		240
Glu Lys Lys Asp Leu Asn Val Gly Trp Val His Arg Asp Gly Lys Arg						
		245		250		255
Tyr Phe Phe Asn Asn Arg Glu Glu Gln Val Gly Thr Glu His Ala Lys						
		260		265		270
Lys Val Ile Asp Ile Ser Glu His Asn Gly Arg Ile Asn Asp Trp Lys						
		275		280		285
Lys Val Ile Asp Glu Asn Glu Val Asp Gly Val Ile Val Arg Leu Gly						
		290		295		300
Tyr Ser Gly Lys Glu Asp Lys Glu Leu Ala His Asn Ile Lys Glu Leu						
		305		310		315
Asn Arg Leu Gly Ile Pro Tyr Gly Val Tyr Leu Tyr Thr Tyr Ala Glu						
		325		330		335
Asn Glu Thr Asp Ala Glu Ser Asp Ala Lys Gln Thr Ile Glu Leu Ile						
		340		345		350
Lys Lys Tyr Asn Met Asn Leu Ser Tyr Pro Ile Tyr Tyr Asp Val Glu						
		355		360		365
Asn Trp Glu Tyr Val Asn Lys Ser Lys Arg Ala Pro Ser Asp Thr Gly						
		370		375		380
Thr Trp Val Lys Ile Ile Asn Lys Tyr Met Asp Thr Met Lys Gln Ala						
		385		390		395
Gly Tyr Gln Asn Val Tyr Val Tyr Ser Tyr Arg Ser Leu Leu Gln Thr						
		405		410		415
Arg Leu Lys His Pro Asp Ile Leu Lys His Val Asn Trp Val Ala Ala						
		420		425		430
Tyr Thr Asn Ala Leu Glu Trp Glu Asn Pro His Tyr Ser Gly Lys Lys						
		435		440		445
Gly Trp Gln Tyr Thr Ser Ser Glu Tyr Met Lys Gly Ile Gln Gly Arg						
		450		455		460
Val Asp Val Ser Val Trp Tyr						
		465		470		

## (2) INFORMATION FOR SEQ ID NO: 159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

TACGTCTCAG CCTACTTTTG TAAGAGCAGA AGAATCTCCA CAAGTTGTCTG AAAAATCTTC	60
ATTAGAGAAG AAATATGAGG AAGCAAAAGC AAAAGCTGAT ACTGCCAAGA AAGATTACGA	120

AACGGCTAAA	AAGAAAGCAG	AAGACGCTCA	GAAAAAGTAT	GAAGATGATC	AGAAGAGAAC	180
TGAGGAGAAA	GCTCGAAAAG	AAGCAGAAGC	ATCTCAAAAA	TTGAATGATG	TGGCGCTTGT	240
TGTTCAAAAT	GATATAAAG	AGTACCGAGA	AGTTCAAAAT	CAACGTAGTA	AATATAAATC	300
TGACGCTGAA	TATCAGAAAA	AATTAACAGA	GGTCGACTCT	AAAATAGAGA	AGGCTAGGAA	360
AGAGCAACAG	GACTTGCAAA	ATAAATTTAA	TGAAGTAAGA	GCAGTTGTAG	TTCCTGAACC	420
AAATGCGTTG	GCTGAGACTA	AGAAAAAAGC	AGAAGAAGCT	AAAGCAGAAG	AAAAAGTAGC	480
TAAGAGAAAA	TATGATTATG	CAACTCTAAA	GGTAGCACTA	GCGAAGAAAG	AAGTAGAGGC	540
TAAGGAACTT	GAAATTGAAA	AACTTCAATA	TGAAATTTCT	ACTTTGGAAC	AAGAAGTTGC	600
TACTGCTCAA	CATCAAGTAG	ATAATTTGAA	AAACTTCTT	GCTGGTGCGG	ATCCTGATGA	660
TGGCACAGAA	GTTATAGAAG	CTAAATTTAA	AAAAGGAGAA	GCTGAGCTAA	ACGCTAAACA	720
AGCTGAGTTA	GCAAAAAAAC	AAACAGAACT	TGAAAAACTT	CTTGACAGCC	TTGATCCTGA	780
AGGTAAGACT	CAGGATGAAT	TAGATAAAGA	AGCAGAAGAA	GCTGAGTTGG	ATAAAAAAGC	840
TGATGAACTT	CAAATAAAG	TTGCTGATTT	AGAAAAAGAA	ATTAGTAACC	TTGAAATATT	900
ACTTGGAGGG	GCTGATNCTG	AAGATGATAC	TGCTGCTCTT	CAAATAAAT	TAGCTACTAA	960
AAAAGCTGAA	TTGGAAAAAA	CTCAAAAAGA	ATTAGATGCA	GCTCTTAATG	AGTTAGGCCC	1020
TGATGGAGAT	GAAGAAGAAA	CTCCAGCGCC	GGCTCCTCAA	CCAGAGCAAC	CAGCTCCTGC	1080
ACCAAAACCA	GAGCAACCAG	CTCCAGCTCC	AAAACCAGAG	CAACCAGCTC	CTGCACCAAA	1140
ACCAGAGCAA	CCAGCTCCAG	CTCCAAAACC	AGAGCAACCA	GCTCCAGCTC	CAAAACCAGA	1200
GCAACCAGCT	AAGCCGGAGA	AACCAGCTGA	AGAGCCTACT	CAACCAGAAA	AACCAGCCAC	1260
TCCAAAAACA	GGCTGGAAAC	AAGAAAACGG	TATGTGGTAT	TTCTACAATA	CTGATGGTTC	1320
AATGGCAATA	GGTTGGCTCC	AAAACAACGG	TTCATGGTAC	TACCTAAACG	CTAACGGCGC	1380
TATGGCAACA	GGTTGGGTGA	AAGATGGAGA	TACCTGGTAC	TATCTTGAAG	CATCAGGTGC	1440
TATGAAAGCA	AGCCAATGGT	TCAAAGTATC	AGATAAATGG	TACTATGTCA	ACAGCAATGG	1500
CGCTATGGCG	ACAGGCTGGC	TCCAATACAA	TGGCTCATGG	TACTACCTCA	ACGCTAATGG	1560
TGATATGGCG	ACAGGATGGC	TCCAATACAA	CGGTTTCATGG	TATTACCTCA	ACGCTAATGG	1620
TGATATGGCG	ACAGGATGGG	CTAAAGTCAA	CGGTTTCATGG	TACTACCTAA	ACGCTAACGG	1680
TGCTATGGCT	ACAGGTTGGG	CTAAAGTCAA	CGGTTTCATGG	TACTACCTAA	ACGCTAACGG	1740
TTCAATGGCA	ACAGGTTGGG	TGAAAGATGG	AGATACCTGG	TACTATCTTG	AAGCATCAGG	1800
TGCTATGAAA	GCAAGCCAAT	GGTTCAAAGT	ATCAGATAAA	TGGTACTATG	TCAATGGCTT	1860
AGGTGCCCTT	GCAGTCAACA	CAACTGTAGA	TGGCTATAAA	GTCAATGCCA	ATGGTGAATG	1920
GGTT						1924

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

Thr Ser Gln Pro Thr Phe Val Arg Ala Glu Glu Ser Pro Gln Val Val
1      5      10      15
Glu Lys Ser Ser Leu Glu Lys Lys Tyr Glu Glu Ala Lys Ala Lys Ala
20      25      30
Asp Thr Ala Lys Lys Asp Tyr Glu Thr Ala Lys Lys Lys Ala Glu Asp
35      40      45
Ala Gln Lys Lys Tyr Glu Asp Asp Gln Lys Arg Thr Glu Glu Lys Ala
50      55      60
Arg Lys Glu Ala Glu Ala Ser Gln Lys Leu Asn Asp Val Ala Leu Val
65      70      75      80
Val Gln Asn Ala Tyr Lys Glu Tyr Arg Glu Val Gln Asn Gln Arg Ser
85      90      95
Lys Tyr Lys Ser Asp Ala Glu Tyr Gln Lys Lys Leu Thr Glu Val Asp
100     105     110
Ser Lys Ile Glu Lys Ala Arg Lys Glu Gln Gln Asp Leu Gln Asn Lys
115     120     125
Phe Asn Glu Val Arg Ala Val Val Val Pro Glu Pro Asn Ala Leu Ala
130     135     140
Glu Thr Lys Lys Lys Ala Glu Glu Ala Lys Ala Glu Glu Lys Val Ala
145     150     155     160
Lys Arg Lys Tyr Asp Tyr Ala Thr Leu Lys Val Ala Leu Ala Lys Lys
165     170     175
Glu Val Glu Ala Lys Glu Leu Glu Ile Glu Lys Leu Gln Tyr Glu Ile
180     185     190
Ser Thr Leu Glu Gln Glu Val Ala Thr Ala Gln His Gln Val Asp Asn
195     200     205
Leu Lys Lys Leu Leu Ala Gly Ala Asp Pro Asp Asp Gly Thr Glu Val
210     215     220
Ile Glu Ala Lys Leu Lys Lys Gly Glu Ala Glu Leu Asn Ala Lys Gln
225     230     235     240
Ala Glu Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys Leu Leu Asp Ser
245     250     255
Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu Leu Asp Lys Glu Ala Glu
260     265     270

```

09765272.012201

Glu Ala Glu Leu Asp Lys Lys Ala Asp Glu Leu Gln Asn Lys Val Ala  
 275 280 285  
 Asp Leu Glu Lys Glu Ile Ser Asn Leu Glu Ile Leu Leu Gly Gly Ala  
 290 295 300  
 Asp Xaa Glu Asp Asp Thr Ala Ala Leu Gln Asn Lys Leu Ala Thr Lys  
 305 310 315 320  
 Lys Ala Glu Leu Glu Lys Thr Gln Lys Glu Leu Asp Ala Ala Leu Asn  
 325 330 335  
 Glu Leu Gly Pro Asp Gly Asp Glu Glu Glu Thr Pro Ala Pro Ala Pro  
 340 345 350  
 Gln Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro  
 355 360 365  
 Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro  
 370 375 380  
 Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu  
 385 390 395 400  
 Gln Pro Ala Lys Pro Glu Lys Pro Ala Glu Glu Pro Thr Gln Pro Glu  
 405 410 415  
 Lys Pro Ala Thr Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp  
 420 425 430  
 Tyr Phe Tyr Asn Thr Asp Gly Ser Met Ala Ile Gly Trp Leu Gln Asn  
 435 440 445  
 Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly  
 450 455 460  
 Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala  
 465 470 475 480  
 Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val  
 485 490 495  
 Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser  
 500 505 510  
 Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Leu Gln  
 515 520 525  
 Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr  
 530 535 540  
 Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly  
 545 550 555 560  
 Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu  
 565 570 575  
 Asn Ala Asn Gly Ser Met Ala Thr Gly Trp Val Lys Asp Gly Asp Thr  
 580 585 590  
 Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser Gln Trp Phe  
 595 600 605

09765272.012201

Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala  
 610 615 620

Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp  
 625 630 635 640

Val

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

TGGACAGGTG AAAGGTCATG CTACATTTGT GAAATCCATG ACAACTGAAA TGTACCAAGA 60  
 ACAACAGAAC CATTCTCTCG CCTACAATCA ACGCTTGGNT TCGCAAAAATC GCATTGTAGA 120  
 TCCTTTTTTTG GCGGAGGGAT ATGAGGTCAA TTACCAAGTG TCTGACGACC CTGATGCAGT 180  
 CTATGGTTAC TTGTCTATTC CAAGTTTGA AATCATGGAG CCGGTTTATT TGGGAGCAGA 240  
 TTATCATCAT TTAGGGATGG GCTTGGCTCA TGTGGATGGT ACACCGCTGC CTCTGGATGG 300  
 TACAGGGATT CGCTCAGTGA TTGCTGGGCA CCGTGCAGAG CCAAGCCATG TCTTTTCCG 360  
 CCATTGGAT CAGCTAAAAG TTGGAGATGC TCTTTATTAT GATAATGGCC AGGAAATTGT 420  
 AGAATATCAG ATGATGGACA CAGAGATTAT TTTACCGTCG GAATGGGAAA AATTAGAATC 480  
 GGTTAGCTCT AAAAATATCA TGACCTTGAT AACCTGCGAT CCGATTCCTA CCTTTAATAA 540  
 ACGCTTATTA GTGAATTTTG AACGAGTCGC TGTTTATCAA AAATCAGATC CACAAACAGC 600  
 TGCAGTTGCG AGGGTTGCTT TTACGAAAGA AGGACAATCT GTATCGCGTG TTGCAACCTC 660  
 TCAATGGTTG 670

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Gly Gln Val Lys Gly His Ala Thr Phe Val Lys Ser Met Thr Thr Glu  
 1 5 10 15  
 Met Tyr Gln Glu Gln Gln Asn His Ser Leu Ala Tyr Asn Gln Arg Leu  
 20 25 30

09765272-012201

Xaa Ser Gln Asn Arg Ile Val Asp Pro Phe Leu Ala Glu Gly Tyr Glu  
 35 40 45  
 Val Asn Tyr Gln Val Ser Asp Asp Pro Asp Ala Val Tyr Gly Tyr Leu  
 50 55 60  
 Ser Ile Pro Ser Leu Glu Ile Met Glu Pro Val Tyr Leu Gly Ala Asp  
 65 70 75 80  
 Tyr His His Leu Gly Met Gly Leu Ala His Val Asp Gly Thr Pro Leu  
 85 90 95  
 Pro Leu Asp Gly Thr Gly Ile Arg Ser Val Ile Ala Gly His Arg Ala  
 100 105 110  
 Glu Pro Ser His Val Phe Phe Arg His Leu Asp Gln Leu Lys Val Gly  
 115 120 125  
 Asp Ala Leu Tyr Tyr Asp Asn Gly Gln Glu Ile Val Glu Tyr Gln Met  
 130 135 140  
 Met Asp Thr Glu Ile Ile Leu Pro Ser Glu Trp Glu Lys Leu Glu Ser  
 145 150 155 160  
 Val Ser Ser Lys Asn Ile Met Thr Leu Ile Thr Cys Asp Pro Ile Pro  
 165 170 175  
 Thr Phe Asn Lys Arg Leu Leu Val Asn Phe Glu Arg Val Ala Val Tyr  
 180 185 190  
 Gln Lys Ser Asp Pro Gln Thr Ala Ala Val Ala Arg Val Ala Phe Thr  
 195 200 205  
 Lys Glu Gly Gln Ser Val Ser Arg Val Ala Thr Ser Gln Trp Leu  
 210 215 220

## (2) INFORMATION FOR SEQ ID NO: 163:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

GATTGCTCCT TTGAAGGATT TGAGAGAAAC CATGTTGGAA ATTGCTTCTG GTGCTCAAAA	60
TCTTCGTGCC AAGGAAGTTG GTGCCTATGA ACTGAGAGAA GTAACGCGCC AATTTAATGC	120
TATGTTGGAT CAGATTGATC AGTTGATGGT AGCTATTCGT AGCCAGGAAG AAACGACCCG	180
TCAGTACCAA CTTCAAGCCC TTTCGAGCCA GATTAATCCA CATTCCTCT ATAACACTTT	240
GGACACCATC ATCTGGATGG CTGAATTTCA TGATAGTCAG CGAGTGGTGC AGGTGACCAA	300
GTCCTTGGCA ACCTATTTCC GATTGGGCGT CAATCAAGGC AAGGACTTGA TTTGTCTCTC	360
TGACGAAATC AATCATGTCC GCCAGTATCT CTTTATCCAG AAACAACGCT ATGGAGATAA	420

GCTGGAATAC GAAATTAATG AAAATGTTGC CTTTGATAAT TTAGTCTTAC CCAAGCTGGT 480  
 CCTACAACCC CTTGTAGAAA ATGCTCTTTA CCATGGCATT AAGGAAAAGG AAGGTCAGGG 540  
 CCATATTAAA CTTTCTGTCC AGAAACAGGA TTCGGGATTG GTCATCCGTA TTGAGGATGA 600  
 TGGCGTTGGC TTCCAAGATG CTGGTGATAG TAGTCAAAGT CAACTCAAAC GTGGGGGAGT 660  
 TGGTCTTCAA AATGTCGATC AACGGCTCAA ACTTCATTTT GGAGCCAATT ACCATATGAA 720  
 GATTGATTCT AGACCCCAAA AAGGGACGAA AGTTGAAATA TATATAAATA GAATAGAAAC 780  
 TAGC 784

## (2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 261 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ile Ala Pro Leu Lys Asp Leu Arg Glu Thr Met Leu Glu Ile Ala Ser  
 1 5 10 15  
 Gly Ala Gln Asn Leu Arg Ala Lys Glu Val Gly Ala Tyr Glu Leu Arg  
 20 25 30  
 Glu Val Thr Arg Gln Phe Asn Ala Met Leu Asp Gln Ile Asp Gln Leu  
 35 40 45  
 Met Val Ala Ile Arg Ser Gln Glu Glu Thr Thr Arg Gln Tyr Gln Leu  
 50 55 60  
 Gln Ala Leu Ser Ser Gln Ile Asn Pro His Phe Leu Tyr Asn Thr Leu  
 65 70 75 80  
 Asp Thr Ile Ile Trp Met Ala Glu Phe His Asp Ser Gln Arg Val Val  
 85 90 95  
 Gln Val Thr Lys Ser Leu Ala Thr Tyr Phe Arg Leu Ala Leu Asn Gln  
 100 105 110  
 Gly Lys Asp Leu Ile Cys Leu Ser Asp Glu Ile Asn His Val Arg Gln  
 115 120 125  
 Tyr Leu Phe Ile Gln Lys Gln Arg Tyr Gly Asp Lys Leu Glu Tyr Glu  
 130 135 140  
 Ile Asn Glu Asn Val Ala Phe Asp Asn Leu Val Leu Pro Lys Leu Val  
 145 150 155 160  
 Leu Gln Pro Leu Val Glu Asn Ala Leu Tyr His Gly Ile Lys Glu Lys  
 165 170 175  
 Glu Gly Gln Gly His Ile Lys Leu Ser Val Gln Lys Gln Asp Ser Gly  
 180 185 190

09765272.012201



Leu Val Ile Arg Ile Glu Asp Asp Gly Val Gly Phe Gln Asp Ala Gly  
 195 200 205

Asp Ser Ser Gln Ser Gln Leu Lys Arg Gly Gly Val Gly Leu Gln Asn  
 210 215 220

Val Asp Gln Arg Leu Lys Leu His Phe Gly Ala Asn Tyr His Met Lys  
 225 230 235 240

Ile Asp Ser Arg Pro Gln Lys Gly Thr Lys Val Glu Ile Tyr Ile Asn  
 245 250 255

Arg Ile Glu Thr Ser  
 260

## (2) INFORMATION FOR SEQ ID NO: 165:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TAGGTCATAT GGGACTTTTT TTCTACAACA AAATAGGCTC CATAATATCT ATAAGGGATT	60
TACCCACTAC AAATATTATA GAGCCGAAAA TTCACATCTA ATATATGCAG ACTACTTTGA	120
AATGAAATTA AAAAAATTAT TAAAGGATGA CACAAAAGTT TTTGAAAAAT CTACATTCAA	180
ATTTGTAGAA GGATATAAAA TATACCTGAC AGAATCTAAA GAATCTGGAA TTAAACAAAT	240
GGACAATGTC ATAAAATATT TTGAGTTTAT TGAATCTAAA AGTATTGCTT TATATTTTCA	300
AAAACGATTA AATGAGCTGA TAGAT	325

## (2) INFORMATION FOR SEQ ID NO:166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Arg Ser Tyr Gly Thr Phe Phe Leu Gln Gln Asn Arg Leu His Asn Ile	1 5 10 15
Tyr Lys Gly Phe Thr His Tyr Lys Tyr Tyr Arg Ala Glu Asn Ser His	20 25 30
Leu Ile Tyr Ala Asp Tyr Phe Glu Met Lys Leu Lys Lys Leu Leu Lys	35 40 45
Asp Asp Thr Lys Val Phe Glu Lys Ser Thr Phe Lys Phe Val Glu Gly	50 55 60

09765272.012201

Tyr Lys Ile Tyr Leu Thr Glu Ser Lys Glu Ser Gly Ile Lys Gln Met  
65 70 75 80

Asp Asn Val Ile Lys Tyr Phe Glu Phe Ile Glu Ser Lys Ser Ile Ala  
85 90 95

Leu Tyr Phe Gln Lys Arg Leu Asn Glu Leu Ile Asp  
100 105

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CAACGTTGAG AATTATTTGC GAATGTGTTT GGATAGCATT CAGAATCAGA CGTATCAAAA	60
TTTTGAGTGT TTATTAATCA ATGATGGCTC TCCAGATCAT TCATCCAAAA TATGTGAAGA	120
ATTTGTAGAG AAAGATTCTC GTTTCAAATA TTTTGAGAAA GCAAACGGCG GTCTTTCATC	180
AGCTCGTAAC CTAGGTATTG AATGTTCTGGG GGGGGGCGTA CATTACTTTT GTAGACTC	238

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn Val Glu Asn Tyr Leu Arg Met Cys Leu Asp Ser Ile Gln Asn Gln	1 5 10 15
Thr Tyr Gln Asn Phe Glu Cys Leu Leu Ile Asn Asp Gly Ser Pro Asp	20 25 30
His Ser Ser Lys Ile Cys Glu Glu Phe Val Glu Lys Asp Ser Arg Phe	35 40 45
Lys Tyr Phe Glu Lys Ala Asn Gly Gly Leu Ser Ser Ala Arg Asn Leu	50 55 60
Gly Ile Glu Cys Ser Gly Gly Gly Val His Tyr Phe Cys Arg Leu	65 70 75

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid

0076527E.012200

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

CTACTATCAA TCAAGTTCTT CAGCCATTGA GGCCACCATT GAGGGCAACA GCCAAACGAC 60  
CATCAGCCAG ACTAGCCACT TTATTGAGTC TTATATCAAA AACTAGAAA CCACCTCGAC 120  
TGGTTTGACC CAGCAGACGG ATGTTCTGGC CTATGCTGAG AATCCCAGTC AAGACAAGGT 180  
CGAGGGAATC CGAGATTTGT TTTTGACCAT CTTGAAGTCA GATAAGGACT TGAAAACGT 240  
TGTGCTGGTG ACCAAATCTG GTCAGGTCAT TTCTACAGAT GACAGTGTGC AGATGAAAAC 300  
TTCCTCTGAT ATGATGGCTG AGGATTGGTA CCAAAGGCC ATTCATCAGG GAGCTATGCC 360  
TGTTTTGACT CCAGCTCGTA AATCAGATAG TCAGTGGGTC ATTTCTGTCA CTCAAGAACT 420  
TGTTGATGCA AAGGGAGCCA ATCTTGGTGT GCTTCGTTTG GATATTTCTT ATGAAACTCT 480  
GGAAGCCTAT CTCAATCAAC TCCAGTTGGG GCAGCAGGGC TTTGCCTTCA TTATCAATGA 540  
AAACCATGAA TTTGTCTACC ATCCTCAACA CACAGTTTAT AGTTCGTCTA GCAAATGGA 600  
GGCTATGAAA CCCTACATCG ATACAGGTCA GGGTTATACT CCTGGTCACA AATCCTACGT 660  
CAGTCAAGAG AAGATTGCAG GAACTGATTG GACGGTGCTT GCGGTGTCAT CATTGGAAAA 720  
GTTAGACCAG GTTCGGAGTC AG 742

## (2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Tyr Tyr Gln Ser Ser Ser Ser Ala Ile Glu Ala Thr Ile Glu Gly Asn  
1 5 10 15  
Ser Gln Thr Thr Ile Ser Gln Thr Ser His Phe Ile Gln Ser Tyr Ile  
20 25 30  
Lys Lys Leu Glu Thr Thr Ser Thr Gly Leu Thr Gln Gln Thr Asp Val  
35 40 45  
Leu Ala Tyr Ala Glu Asn Pro Ser Gln Asp Lys Val Glu Gly Ile Arg  
50 55 60  
Asp Leu Phe Leu Thr Ile Leu Lys Ser Asp Lys Asp Leu Lys Thr Val  
65 70 75 80  
Val Leu Val Thr Lys Ser Gly Gln Val Ile Ser Thr Asp Asp Ser Val  
85 90 95

00765272.012201

Gln Met Lys Thr Ser Ser Asp Met Met Ala Glu Asp Trp Tyr Gln Lys  
 100 105 110  
 Ala Ile His Gln Gly Ala Met Pro Val Leu Thr Pro Ala Arg Lys Ser  
 115 120 125  
 Asp Ser Gln Trp Val Ile Ser Val Thr Gln Glu Leu Val Asp Ala Lys  
 130 135 140  
 Gly Ala Asn Leu Gly Val Leu Arg Leu Asp Ile Ser Tyr Glu Thr Leu  
 145 150 155 160  
 Glu Ala Tyr Leu Asn Gln Leu Gln Leu Gly Gln Gln Gly Phe Ala Phe  
 165 170 175  
 Ile Ile Asn Glu Asn His Glu Phe Val Tyr His Pro Gln His Thr Val  
 180 185 190  
 Tyr Ser Ser Ser Ser Lys Met Glu Ala Met Lys Pro Tyr Ile Asp Thr  
 195 200 205  
 Gly Gln Gly Tyr Thr Pro Gly His Lys Ser Tyr Val Ser Gln Glu Lys  
 210 215 220  
 Ile Ala Gly Thr Asp Trp Thr Val Leu Gly Val Ser Ser Leu Glu Lys  
 225 230 235 240  
 Leu Asp Gln Val Arg Ser Gln  
 245

## (2) INFORMATION FOR SEQ ID NO: 171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GACAAAAACA TTAAAACGTC CTGAGGTTTT ATCACCTGCA GGGACTTTAG AGAAGCTAAA	60
GGTAGCTGTT CAGTATGGAG CAGATGCTGT CTTTATCGGT GGTCAGGCCT ATGGTCTTCG	120
TAGCCGTGCG GGAAACTTTA CTTTCGAACA GATGGAAGAA GCGGTGCAGT TTGCGGCCAA	180
GTATGGTGCC AAGGTCTATG TAGCGGCTAA TATGGTTATG CACGAAGGAA ATGAAGCTGG	240
TGCTGGTGAG TGGTTCGTA AACTGCGTGA TATCGGGATT GCAGCAGTTA TCGTATCTGA	300
CCCAGCCTTG ATTATGATTG CAGTGA CTGA AGCACCAGGC CTTGAAATCC ACCTTTCTAC	360
CCAAGCCAGT GCCACTAACT ATGAAACCCT TGAGTTCTGG AAAGAGCTAG GCTTGACTCG	420
TGTCGTTTTA GCGCGTGAGG TTTCAATGGA AGAATTAGCT GAGATCCGCA AACGTACAGA	480
TGTTGAAATT GAAGCCTTTG TCCATGGAGC TATGTGTATT TCATACTCTG GACGTTGTAC	540
TCTTTCAAAC CACATGAGTA TGC GTGATGC CAACCGTGGT GGATGTTCTC AGTCATGCCG	600

00765072 012201

TTGGAAATAC GACCTTTACG ATATGCCATT TGGGAAAGAA CGTAAGAGTT TGCAGGGTGA 660  
 GATTCCAGAA GAATTTTCAA TGTCAGCCGT TGACATGTCT ATGATTGACC ANATTCCAGA 720  
 TATGATTGAA AATGGTGTGG ACAGTCTAAA AATCGAAGGA CGTATGNAGT CTATTCTACTA 780  
 NGTATCAACA GTAACCAACT GCTACAAGGC GGCTGTGGAT GCCTATCTTG AAAGTCCTGA 840  
 AAAGTTTGAA GCTATCAAAC AAGACTTGGT GGACGAGATG TGGAAGGTTG CCCAACGTGA 900  
 ACTGGCTACA GGATTTTACT ATGGTACACC ATCTGAAAAT GAGCAGTTGT TTGGTGCTCG 960  
 TCGTAAATC CCTGAGTACA AGTTTGTGCG TGAAGTGGTT TCTTATGATG ATGCGGCACA 1020  
 AACAGCAACT ATTCGTCAAC GAAACGTCAT TAACGAAGGG GACCAAGTTG AGTTTTATGG 1080  
 TCCAGGTTTC CGTCATTTTG AAACCTATAT TGAAGATTG CATGATGCTA AAGGCAATAA 1140  
 AATCGACCGC GCTCCAAATC CAATGGAAC ATTGACTATT AAAGTCCCAC AACCTGTTCA 1200  
 ATCAGGAGAC ATGGTTCGAG CTCTTAAAGA GGGGCTTATC AATCTTTATA AGGAAGATGG 1260  
 AACCAGCGTC ACAGTTCGTG CT 1282

## (2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Thr Lys Thr Leu Lys Arg Pro Glu Val Leu Ser Pro Ala Gly Thr Leu  
 1 5 10 15  
 Glu Lys Leu Lys Val Ala Val Gln Tyr Gly Ala Asp Ala Val Phe Ile  
 20 25 30  
 Gly Gly Gln Ala Tyr Gly Leu Arg Ser Arg Ala Gly Asn Phe Thr Phe  
 35 40 45  
 Glu Gln Met Glu Glu Gly Val Gln Phe Ala Ala Lys Tyr Gly Ala Lys  
 50 55 60  
 Val Tyr Val Ala Ala Asn Met Val Met His Glu Gly Asn Glu Ala Gly  
 65 70 75 80  
 Ala Gly Glu Trp Phe Arg Lys Leu Arg Asp Ile Gly Ile Ala Ala Val  
 85 90 95  
 Ile Val Ser Asp Pro Ala Leu Ile Met Ile Ala Val Thr Glu Ala Pro  
 100 105 110  
 Gly Leu Glu Ile His Leu Ser Thr Gln Ala Ser Ala Thr Asn Tyr Glu  
 115 120 125  
 Thr Leu Glu Phe Trp Lys Glu Leu Gly Leu Thr Arg Val Val Leu Ala  
 130 135 140

09765272.012201

Arg Glu Val Ser Met Glu Glu Leu Ala Glu Ile Arg Lys Arg Thr Asp  
 145 150 155 160  
 Val Glu Ile Glu Ala Phe Val His Gly Ala Met Cys Ile Ser Tyr Ser  
 165 170 175  
 Gly Arg Cys Thr Leu Ser Asn His Met Ser Met Arg Asp Ala Asn Arg  
 180 185 190  
 Gly Gly Cys Ser Gln Ser Cys Arg Trp Lys Tyr Asp Leu Tyr Asp Met  
 195 200 205  
 Pro Phe Gly Lys Glu Arg Lys Ser Leu Gln Gly Glu Ile Pro Glu Glu  
 210 215 220  
 Phe Ser Met Ser Ala Val Asp Met Ser Met Ile Asp Xaa Ile Pro Asp  
 225 230 235 240  
 Met Ile Glu Asn Gly Val Asp Ser Leu Lys Ile Glu Gly Arg Met Xaa  
 245 250 255  
 Ser Ile His Xaa Val Ser Thr Val Thr Asn Cys Tyr Lys Ala Ala Val  
 260 265 270  
 Asp Ala Tyr Leu Glu Ser Pro Glu Lys Phe Glu Ala Ile Lys Gln Asp  
 275 280 285  
 Leu Val Asp Glu Met Trp Lys Val Ala Gln Arg Glu Leu Ala Thr Gly  
 290 295 300  
 Phe Tyr Tyr Gly Thr Pro Ser Glu Asn Glu Gln Leu Phe Gly Ala Arg  
 305 310 315 320  
 Arg Lys Ile Pro Glu Tyr Lys Phe Val Ala Glu Val Val Ser Tyr Asp  
 325 330 335  
 Asp Ala Ala Gln Thr Ala Thr Ile Arg Gln Arg Asn Val Ile Asn Glu  
 340 345 350  
 Gly Asp Gln Val Glu Phe Tyr Gly Pro Gly Phe Arg His Phe Glu Thr  
 355 360 365  
 Tyr Ile Glu Asp Leu His Asp Ala Lys Gly Asn Lys Ile Asp Arg Ala  
 370 375 380  
 Pro Asn Pro Met Glu Leu Leu Thr Ile Lys Val Pro Gln Pro Val Gln  
 385 390 395 400  
 Ser Gly Asp Met Val Arg Ala Leu Lys Glu Gly Leu Ile Asn Leu Tyr  
 405 410 415  
 Lys Glu Asp Gly Thr Ser Val Thr Val Arg Ala  
 420 425

## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

09765272.012201

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TTCTCAGGAG ACCTTTAAAA ATATCACCAA TAGCTTCTCC ATGCAAATCA-ATCGTCGCGT 60  
 CAACCAAGGA ACGCCTCGTG GTGCTGGGAA TATCAAGGGT GAAGACATCA AAAAAATCAC 120  
 CGAAAACAAG GCCATTGAGT CTTATGTCAA ACGTATCAAC GCTATCGGAG ATTTGACTGG 180  
 ATATGACCTG ATTGAAACGC CAGAAACCAA GAAGAATCTC ACTGCTGATC GTGCCAAGCG 240  
 TTTTGGAAGT AGCTTGATGA TTACAGGTGT CAATGACTCC TCTAAAGAAG ACAAGTTTGT 300  
 CTCTGGTTCT TATAAACTAG TCGAAGGAGA GCACTTAACC AACGACGACA AGGATAAAAT 360  
 CCTCTTGCAC AAGGACTTGG CAGCCAAACA CGGCTGGAAA GTAGGGGACA AGGTAAACT 420  
 GGACTCTAAT ATCTACGATG CAGATAATGA AAAAGGAGCC AAGGAAACAG TTGAAGTGAC 480  
 AATCAAGGGA CTCTTTGATG GTCATAATAA GTCAGCAGTA ACCTACTCAC AAGAACTTTA 540  
 CGAAAACACA GCTATTACAG ACATTCACAC TGCTGCAAAA CTTTATGGAT ACACAGAAGA 600  
 CACAGCCATT TATGGGGACG CAACCTTCTT TGTAACAGCA GACAAGAACT TGGATGATGT 660  
 TATGAAAGAG TTGAATGGCA TCAGTGGTAT CAACTGGAAG AGCTACACAC TCGTCAAGAG 720  
 CTCCTCTAAC TACCCAGCTC TTGAGCAATC TATCTCTGGT ATGTACAAGA TGGCCAAC 778

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser Gln Glu Thr Phe Lys Asn Ile Thr Asn Ser Phe Ser Met Gln Ile  
 1 5 10 15  
 Asn Arg Arg Val Asn Gln Gly Thr Pro Arg Gly Ala Gly Asn Ile Lys  
 20 25 30  
 Gly Glu Asp Ile Lys Lys Ile Thr Glu Asn Lys Ala Ile Glu Ser Tyr  
 35 40 45  
 Val Lys Arg Ile Asn Ala Ile Gly Asp Leu Thr Gly Tyr Asp Leu Ile  
 50 55 60  
 Glu Thr Pro Glu Thr Lys Lys Asn Leu Thr Ala Asp Arg Ala Lys Arg  
 65 70 75 80  
 Phe Gly Ser Ser Leu Met Ile Thr Gly Val Asn Asp Ser Ser Lys Glu  
 85 90 95  
 Asp Lys Phe Val Ser Gly Ser Tyr Lys Leu Val Glu Gly Glu His Leu  
 100 105 110

00765272.012201  
 102210" 2259260

Thr Asn Asp Asp Lys Asp Lys Ile Leu Leu His Lys Asp Leu Ala Ala  
 115 120 125  
 Lys His Gly Trp Lys Val Gly Asp Lys Val Lys Leu Asp Ser Asn Ile  
 130 135 140  
 Tyr Asp Ala Asp Asn Glu Lys Gly Ala Lys Glu Thr Val Glu Val Thr  
 145 150 155 160  
 Ile Lys Gly Leu Phe Asp Gly His Asn Lys Ser Ala Val Thr Tyr Ser  
 165 170 175  
 Gln Glu Leu Tyr Glu Asn Thr Ala Ile Thr Asp Ile His Thr Ala Ala  
 180 185 190  
 Lys Leu Tyr Gly Tyr Thr Glu Asp Thr Ala Ile Tyr Gly Asp Ala Thr  
 195 200 205  
 Phe Phe Val Thr Ala Asp Lys Asn Leu Asp Asp Val Met Lys Glu Leu  
 210 215 220  
 Asn Gly Ile Ser Gly Ile Asn Trp Lys Ser Tyr Thr Leu Val Lys Ser  
 225 230 235 240  
 Ser Ser Asn Tyr Pro Ala Leu Glu Gln Ser Ile Ser Gly Met Tyr Lys  
 245 250 255  
 Met Ala Asn

## (2) INFORMATION FOR SEQ ID NO: 175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AGTAAATGCG CAATCAAATT CATTAATATT AATAGATGAA CCTGAAATCT CACTTCATCC	60
GAGTGCAATC TATAAATTTA AAGAGTTTTT ACTTCAAGAG TGTTTAAATA AAAAACATCA	120
AATTATTATC ACTACACATT CTACACAACT TATAAAAGAT TTTCCTAGAG AAGCCGTGAA	180
ACTTTTAGTG AAAACGGAG AAAAGGTAGA TGTTATTGAA AATATTGATT ATCAGGATGC	240
ATTTTTTGAA TTAGGTGATG TGTATCATTC TAGGAAGATG ATTTATGTTG AAGATAGACT	300
AGCTAAATAT ATTCTAGAGT TTGTTATCAC TCATTCAGGT AGTGAGAATC TTAAACAGAA	360
TTTAGTAGTG AGATATATTC CTGGTGGAGC AAATCAAATA ATTTGTAATA ATATTTTAAA	420
CTCATCGTAT TTAGATTCCG ATAACCATTA TTTTGGCTT GATGGAGATC AAAACACTAA	480
TGTTAGTGAA TCAAATAATT TAATGAAC TAATTGAAAAT GGTGTTGTTA TATCAGATAA	540
AATTCCTGAA TCAGATAATA AAAATCTTGA TGATATTATA AAATTGATAA NGGGATGTCC	600



AATTAAATTT AATGTTTCAG GTAATAAAGG GCAAAAAAAT AATATTGAAT TAATTGCGAA

660

ACAAAGAAGC TTTATAGATT ATTGGGCTAA ATAC

694

## (2) INFORMATION FOR SEQ ID NO:176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Val	Asn	Ala	Gln	Ser	Asn	Ser	Leu	Ile	Leu	Ile	Asp	Glu	Pro	Glu	Ile	1	5	10	15
Ser	Leu	His	Pro	Ser	Ala	Ile	Tyr	Lys	Phe	Lys	Glu	Phe	Leu	Leu	Gln	20	25	30	
Glu	Cys	Leu	Asn	Lys	Lys	His	Gln	Ile	Ile	Ile	Thr	Thr	His	Ser	Thr	35	40	45	
Gln	Leu	Ile	Lys	Asp	Phe	Pro	Arg	Glu	Ala	Val	Lys	Leu	Leu	Val	Lys	50	55	60	
Asn	Gly	Glu	Lys	Val	Asp	Val	Ile	Glu	Asn	Ile	Asp	Tyr	Gln	Asp	Ala	65	70	75	80
Phe	Phe	Glu	Leu	Gly	Asp	Val	Tyr	His	Ser	Arg	Lys	Met	Ile	Tyr	Val	85	90	95	
Glu	Asp	Arg	Leu	Ala	Lys	Tyr	Ile	Leu	Glu	Phe	Val	Ile	Thr	His	Ser	100	105	110	
Gly	Ser	Glu	Asn	Leu	Lys	Gln	Asn	Leu	Val	Val	Arg	Tyr	Ile	Pro	Gly	115	120	125	
Gly	Ala	Asn	Gln	Ile	Ile	Cys	Asn	Asn	Ile	Leu	Asn	Ser	Ser	Tyr	Leu	130	135	140	
Asp	Ser	Asp	Asn	His	Tyr	Phe	Trp	Leu	Asp	Gly	Asp	Gln	Asn	Thr	Asn	145	150	155	160
Val	Ser	Glu	Ser	Asn	Asn	Leu	Met	Asn	Tyr	Leu	Glu	Asn	Gly	Val	Val	165	170	175	
Ile	Ser	Asp	Lys	Ile	Pro	Glu	Ser	Asp	Asn	Lys	Asn	Leu	Asp	Asp	Ile	180	185	190	
Ile	Lys	Leu	Ile	Xaa	Gly	Cys	Pro	Ile	Lys	Phe	Asn	Val	Ser	Gly	Asn	195	200	205	
Lys	Gly	Gln	Lys	Asn	Asn	Ile	Glu	Leu	Ile	Ala	Lys	Gln	Arg	Ser	Phe	210	215	220	
Ile	Asp	Tyr	Trp	Ala	Lys	Tyr	225	230											

## (2) INFORMATION FOR SEQ ID NO: 177:

00765272.012201

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TTACCGCGTT CATCAAGATG TCAAACAAGT CATGACCTAT CAACCCATGG TCGGAGAAAT 60  
ATTGAGTGAA CAAGACACCC CAGCAAACGA AGAGCTTGTG CTTGCTATGA TTTATACTGA 120  
AACAAAAGGA AAAGAAGGCG ATGTTATGCA GTCTAGTGAG TCTGCAAGTG GTTCCACCAA 180  
CACCATCAAT GATAATGCCT CTAGCATTCTG GCAAGGCATT CAAACTCTGA CAGGCAATCT 240  
CTATCTGGCG CAGAAGAAGG GGGTAGATAT CTGGACAGCT GTTCAAGCCT ATAATTTTGG 300  
ACCTGCCTAT ATCGATTTTA TCGCCCAAAA TGGCAAGGAA AATACCCTGG CTCTAGCCAA 360  
ACAGTACTCT CGTGAGACTG TTGCCCCCTT GCTTGGAAT AGGACTGGAA AGACTTATAG 420  
TTATATTAC CCCATTTCCA TTTTTCACGG TGCTGAACTC TATGTAAATG GAGGAAACTA 480  
TTATTATTCT AGACAGGTAC GACTTAACCT TTACATCATC AAATGTTTCA CTCTCTTTTC 540  
AACATCTGGC 550

## (2) INFORMATION FOR SEQ ID NO:178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Tyr Arg Val His Gln Asp Val Lys Gln Val Met Thr Tyr Gln Pro Met  
1 5 10 15  
Val Arg Glu Ile Leu Ser Glu Gln Asp Thr Pro Ala Asn Glu Glu Leu  
20 25 30  
Val Leu Ala Met Ile Tyr Thr Glu Thr Lys Gly Lys Glu Gly Asp Val  
35 40 45  
Met Gln Ser Ser Glu Ser Ala Ser Gly Ser Thr Asn Thr Ile Asn Asp  
50 55 60  
Asn Ala Ser Ser Ile Arg Gln Gly Ile Gln Thr Leu Thr Gly Asn Leu  
65 70 75 80  
Tyr Leu Ala Gln Lys Lys Gly Val Asp Ile Trp Thr Ala Val Gln Ala  
85 90 95  
Tyr Asn Phe Gly Pro Ala Tyr Ile Asp Phe Ile Ala Gln Asn Gly Lys

284

100

105

110

Glu Asn Thr Leu Ala Leu Ala Lys Gln Tyr Ser Arg Glu Thr Val Ala  
 115 120 125  
 Pro Leu Leu Gly Asn Arg Thr Gly Lys Thr Tyr Ser Tyr Ile His Pro  
 130 135 140  
 Ile Ser Ile Phe His Gly Ala Glu Leu Tyr Val Asn Gly Gly Asn Tyr  
 145 150 155 160  
 Tyr Tyr Ser Arg Gln Val Arg Leu Asn Leu Tyr Ile Ile Lys Cys Phe  
 165 170 175  
 Thr Leu Phe Ser Thr Ser Gly  
 180

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GTGGATGGGC TTAACTATC TTCGTATTCG CCGTGCGGCT AAAATTGTGG ACAATGAGGA 60  
 GTTTGAAGCC TTGATTCGTA CGGGTCAATT GATTGATTG CGCGACCCAG CAGAATTCCA 120  
 CAGAAAACAT ATCCTTGGTG CACGCAATAT TCCTTCAAGT CAGTTGAAAA CTAGTCTTGC 180  
 AGCCCTTCGT AAAGATAAAC CTGTCCTTCT CTACGAAAAC CAACGTGCGC AACGAGTTAC 240  
 AAATGCAGCT CTTTACTTGA AAAACAAGG TTTTCTGAG ATTTATATCC TTTCTTATGG 300  
 CTTGGATTCT TGGAAAGGGA AAGTGAAGAC TAGC 334

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Trp Met Gly Phe Asn Tyr Leu Arg Ile Arg Arg Ala Ala Lys Ile Val  
 1 5 10 15  
 Asp Asn Glu Glu Phe Glu Ala Leu Ile Arg Thr Gly Gln Leu Ile Asp  
 20 25 30  
 Leu Arg Asp Pro Ala Glu Phe His Arg Lys His Ile Leu Gly Ala Arg  
 35 40 45

00765272.012201

Asn Ile Pro Ser Ser Gln Leu Lys Thr Ser Leu Ala Ala Leu Arg Lys  
50 55 60

Asp Lys Pro Val Leu Leu Tyr Glu Asn Gln Arg Ala Gln Arg Val Thr  
65 70 75 80

Asn Ala Ala Leu Tyr Leu Lys Lys Gln Gly Phe Ser Glu Ile Tyr Ile  
85 90 95

Leu Ser Tyr Gly Leu Asp Ser Trp Lys Gly Lys Val Lys Thr Ser  
100 105 110

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ACTAAACCAG CATCGTTCGC AGGAAAATAA GGACAATAAT CGTGTCTCTT ATGTGGATGG	60
CAGCCAGTCA AGTCAGAAAA GTGAAAACCT GACACCAGAC CAGGTTAGCC AGAAAGAAGG	120
AATTCAGGCT GAGCAAATTG TAATCAAAAT TACAGATCAG GGCTATGTAA CGTCACACGG	180
TGACCACTAT CATTACTATA ATGGGAAAGT TCCTTATGAT GCCCTCTTTA GTGAAGAACT	240
CTTGATGAAG GATCCAACT ATCAACTTAA AGACGCTGAT ATTGTCAATG AAGTCAAGGG	300
TGGTTATATC ATCAAGGTCG ATGGAAAATA TTATGTCTAC CTGAAAGATG CAGCTCATGC	360
TGATAATGTT CGAACTAAAG ATGAAATCAA TCGTCAAAAA CAAGAACATG TCAAAGATAA	420
TGAGAAGGTT AACTCTAATG TTGCTGTAGC AAGGTCTCAG GGACGATATA CGACAAATGA	480
TGGTTATGTC TTTAATCCAG CTGATATTAT CGAAGATACG GGTAATGCTT ATATCGTTCC	540
TCATGGAGGT CACTATCACT ACATTCCCAA AAGCGATTTA TCTGCTAGTG AATTAGCAGC	600
AGCTAAAGCA CATCTGGCTG GAAAAAATAT GCAACCGAGT CAGTTAAGCT ATTCTTCAAC	660
AGCTAGTGAC AATAACACGC AATCTGTAGC AAAAGGATCA ACTAGCAAGC CAGCAAATAA	720
ATCTGAAAAT CTCCAGAGTC TTTTGAAGGA ACTCTATGAT TCACCTAGCG CCCAACGTTA	780
CAGTGAATCA GATGGCCTGG TCTTTGACCC TGCTAAGATT ATCAGTCGTA CACCAAATGG	840
AGTTGCGATT CCGCATGGCG ACCATTACCA CTTTATTCCT TACAGCAAGC TTTCTGCCTT	900
AGAAGAAAAG ATTGCCAGAA TGGTGCCTAT CAGTGGAACCT GGTCTACAG TTTCTACAAA	960
TGCAAAACCT AATGAAGTAG TGTCTAGTCT AGGCAGTCTT TCAAGCAATC CTTCTTCTTT	1020
AACGACAAGT AAGGAGCTCT CTTCAGCATC TGATGGTTAT ATTTTAAATC CAAAAGATAT	1080
CGTTGAAGAA ACGGCTACAG CTTATATTGT AAGACATGGT GATCATTTCC ATTACATTCC	1140
AAAATCAAAT CAAATTGGGC AACCGACTCT TCCAAACAAT AGCTAGCAA CACCTTCTCC	1200

ATCTCTTCCA ATCAATCCAG GAACTTCACA TGAGAAACAT GAAGAAGATG GATACGGATT 1260  
 TGATGCTAAT CGTATTATCG CTGAAGATGA ATCAGGTTTT GTCATGAGTC ACGGAGACCA 1320  
 CAATCATTAT TTCTTCAAGA AG 1342

## (2) INFORMATION FOR SEQ ID NO:182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn Asn Arg Val Ser  
 1 5 10 15  
 Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu Asn Leu Thr Pro  
 20 25 30  
 Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu Gln Ile Val Ile  
 35 40 45  
 Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly Asp His Tyr His  
 50 55 60  
 Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe Ser Glu Glu Leu  
 65 70 75 80  
 Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala Asp Ile Val Asn  
 85 90 95  
 Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly Lys Tyr Tyr Val  
 100 105 110  
 Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg Thr Lys Asp Glu  
 115 120 125  
 Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn Glu Lys Val Asn  
 130 135 140  
 Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr Thr Thr Asn Asp  
 145 150 155 160  
 Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp Thr Gly Asn Ala  
 165 170 175  
 Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile Pro Lys Ser Asp  
 180 185 190  
 Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His Leu Ala Gly Lys  
 195 200 205  
 Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr Ala Ser Asp Asn  
 210 215 220  
 Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys Pro Ala Asn Lys

00765272.012201

225		230		235		240
Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr Asp Ser Pro Ser						
	245			250		255
Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe Asp Pro Ala Lys						
	260		265			270
Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro His Gly Asp His						
	275		280			285
Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu Glu Glu Lys Ile						
	290		295			300
Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr Val Ser Thr Asn						
	305		310		315	320
Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser Leu Ser Ser Asn						
		325		330		335
Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser Ala Ser Asp Gly						
		340		345		350
Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr Ala Thr Ala Tyr						
	355		360			365
Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro Lys Ser Asn Gln						
	370		375			380
Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro						
	385		390		395	400
Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu Glu Asp						
		405		410		415
Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu Ser Gly						
	420		425			430
Phe Val Met Ser His Gly Asp His Asn His Tyr Phe Phe Lys Lys						
	435		440			445

## (2) INFORMATION FOR SEQ ID NO: 183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TGACTACCTT GAAATCCCAC TTTACAGCTA TCTTGGTGGA TTCAACACTA AAGTTCTTCC	60
AACTCCAATG ATGAACATCA TCAACGGTGG TTCTCACTCT GACGCTCCAA TCGCTTTCCA	120
AGAGTTCATG ATCTTGCCAG TTGGTGC GCC AACATTTAAA GAAGCCCTTC GTTACGGTGC	180
TGAAATCTTC CACGCTCTTA AGAAAATCCT TAAATCACGT GGT TTG GAAA CTGCCGTAGG	240
TGACGAAGGT GGATTCGCTC CTCGTTTCGA AGGAACTGAA GATGGTGTTG AACTATCCT	300

09765272.012201

TGCTGCGATT GAAGCTGCTG GATATGTACC AGGTAAAGAC GTATTTATCG GATTTGACTG 360  
 TGCTTCATCA GAATTCTACG ATAAAGAACG TAAAGTTTAC GACTACACTA AATTTGAAGG 420  
 TGAAGGTGCT GCTGTTTCGTA CATCTGCAGA ACAAATCGAC TACCTTGAAG AATTGGTTAA 480  
 CAAATACCCA ATCATCACTA TTGAAGATGG TATGGATGAA AACGACTGGG ATGGTTGGAA 540  
 AGCTCTTACT GAACGTCTTG GTAAGAAAGT ACAACTTGTT GGTGACGACT TCTTCGTAAC 600  
 AAACACTGAC TACCTTGCAC GTGGTATCCA AGAAGGTGCT GCTAACTCAA TCCTTATCAA 660  
 AGTTAACCAA ATCGGTACTC TTACTGAAAC TTTTGAAGCT ATCGAAATGG CTAAAGAAGC 720  
 TGGTTACACT GCTGTTGTAT CACACCGTTC AGGTGAAACT GAAGATTCAA CAATCGCTGA 780  
 TATTGCAGTT GCAACTAACG CAGGACAAAT CAAGACTGGT TCACTTTCAC GTACAGACCG 840  
 CATCGCTAAA TACAACCAAT TGCTTCGTAT CGAAGACCAA CTTGGTGAAG TAGCTGAATA 900  
 TCGTGGATTG AAATCATTCT ACAACCTTAA AAAA 934

## (2) INFORMATION FOR SEQ ID NO:184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Asp Tyr Leu Glu Ile Pro Leu Tyr Ser Tyr Leu Gly Gly Phe Asn Thr  
 1 5 10 15  
 Lys Val Leu Pro Thr Pro Met Met Asn Ile Ile Asn Gly Gly Ser His  
 20 25 30  
 Ser Asp Ala Pro Ile Ala Phe Gln Glu Phe Met Ile Leu Pro Val Gly  
 35 40 45  
 Ala Pro Thr Phe Lys Glu Ala Leu Arg Tyr Gly Ala Glu Ile Phe His  
 50 55 60  
 Ala Leu Lys Lys Ile Leu Lys Ser Arg Gly Leu Glu Thr Ala Val Gly  
 65 70 75 80  
 Asp Glu Gly Gly Phe Ala Pro Arg Phe Glu Gly Thr Glu Asp Gly Val  
 85 90 95  
 Glu Thr Ile Leu Ala Ala Ile Glu Ala Ala Gly Tyr Val Pro Gly Lys  
 100 105 110  
 Asp Val Phe Ile Gly Phe Asp Cys Ala Ser Ser Glu Phe Tyr Asp Lys  
 115 120 125  
 Glu Arg Lys Val Tyr Asp Tyr Thr Lys Phe Glu Gly Glu Gly Ala Ala  
 130 135 140  
 Val Arg Thr Ser Ala Glu Gln Ile Asp Tyr Leu Glu Glu Leu Val Asn

09765272.012201

145		150		155		160
Lys Tyr Pro Ile	Ile Thr Ile Glu Asp Gly Met Asp Glu Asn Asp Trp					
	165		170		175	
Asp Gly Trp Lys	Ala Leu Thr Glu Arg Leu Gly Lys Lys Val Gln Leu					
	180		185		190	
Val Gly Asp Asp Phe Phe Val Thr Asn Thr Asp Tyr Leu Ala Arg Gly						
	195		200		205	
Ile Gln Glu Gly Ala Ala Asn Ser Ile Leu Ile Lys Val Asn Gln Ile						
	210		215		220	
Gly Thr Leu Thr Glu Thr Phe Glu Ala Ile Glu Met Ala Lys Glu Ala						
	225		230		235	240
Gly Tyr Thr Ala Val Val Ser His Arg Ser Gly Glu Thr Glu Asp Ser						
	245		250		255	
Thr Ile Ala Asp Ile Ala Val Ala Thr Asn Ala Gly Gln Ile Lys Thr						
	260		265		270	
Gly Ser Leu Ser Arg Thr Asp Arg Ile Ala Lys Tyr Asn Gln Leu Leu						
	275		280		285	
Arg Ile Glu Asp Gln Leu Gly Glu Val Ala Glu Tyr Arg Gly Leu Lys						
	290		295		300	
Ser Phe Tyr Asn Leu Lys Lys						
	305		310			

## (2) INFORMATION FOR SEQ ID NO: 185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

TCGTATCTTT TTTTGGAGCA ATGTTTCGCGT AGAAGGACAT TCCATGGATC CGACCCTAGC	60
GGATGGCGAA ATTCTCTTCG TTGTAAACA CCTTCCTATT GACCGTTTTG ATATCGTGGT	120
GGCCCATGAG GAAGATGGCA ATAAGGACAT CGTCAAGCGC GTGATTGGAA TGCCTGGCGA	180
CACCATTTCGT TACGAAAATG ATAACTCTA CATCAATGAC AAAGAAACGG ACGAGCCTTA	240
TCTAGCAGAC TATATCAAAC GCTTCAAGGA TGACAACTC CAAAGCACTT ACTCAGGCAA	300
GGGCTTTGAA GGAAATAAAG GAACTTTCTT TAGAAGTATC GCTCAAAAAG CTCAAGCCTT	360
CACAGTTGAT GTCAACTACA ACACCAACTT TAGCTTTACT GTTCCAGAAG GAGAATACCT	420
TCTCCTCGGA GATGACCGCT TGGTTTCGAG CGACAGCCGC CACGTAGGTA CCTTCAAAGC	480
AAAAGATATC ACAGGGGAAG CTAAATTCCG CTTATGGCCA ATCACCCGTA TCGGAACATT	540
T	541



## (2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Ile Phe Phe Trp Ser Asn Val Arg Val Glu Gly His Ser Met Asp  
 1                      5                      10                      15  
 Pro Thr Leu Ala Asp Gly Glu Ile Leu Phe Val Val Lys His Leu Pro  
                     20                      25                      30  
 Ile Asp Arg Phe Asp Ile Val Val Ala His Glu Glu Asp Gly Asn Lys  
                     35                      40                      45  
 Asp Ile Val Lys Arg Val Ile Gly Met Pro Gly Asp Thr Ile Arg Tyr  
                     50                      55                      60  
 Glu Asn Asp Lys Leu Tyr Ile Asn Asp Lys Glu Thr Asp Glu Pro Tyr  
                     65                      70                      75                      80  
 Leu Ala Asp Tyr Ile Lys Arg Phe Lys Asp Asp Lys Leu Gln Ser Thr  
                     85                      90                      95  
 Tyr Ser Gly Lys Gly Phe Glu Gly Asn Lys Gly Thr Phe Phe Arg Ser  
                     100                      105                      110  
 Ile Ala Gln Lys Ala Gln Ala Phe Thr Val Asp Val Asn Tyr Asn Thr  
                     115                      120                      125  
 Asn Phe Ser Phe Thr Val Pro Glu Gly Glu Tyr Leu Leu Leu Gly Asp  
                     130                      135                      140  
 Asp Arg Leu Val Ser Ser Asp Ser Arg His Val Gly Thr Phe Lys Ala  
                     145                      150                      155                      160  
 Lys Asp Ile Thr Gly Glu Ala Lys Phe Arg Leu Trp Pro Ile Thr Arg  
                     165                      170                      175  
 Ile Gly Thr Phe  
                     180

## (2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

GGACTCTCTC AAAGATGTGA AAGCAAATGC TAGCGACAGC AAGCCTGCAC AGGACAAGAA

GGATGCAAAA CAAGGAACGG AAGATAGTAA GGATTCAGAT AAGATGACTG AAACAAACTC 120  
 AGTTCCGGCA GGAGTGATTG TGGTCAGTCT ACTTGCCCTC CTAGGCGTGA TTGCCTTCTG 180  
 GCTGATTTCG CGTAAGAAAG AGTCAGAAAT CCAGCAATTA AGCACGGAAT TGATCAAGGT 240  
 TCTAGGACAG CTAGATGCAG AAAAAGCGGA TAAAAAGTC CTTGCCAAAG CCCAAAACCT 300  
 TCTCCAAGAA ACCCTTGATT TCGTGAAAGA AGAAAATGGC TCAGCAGAGA CAGAAACTAA 360  
 ACTAGTAGAG GAGCTTAAAG CAATCCTTGA CAAACTCAAG 400

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Asp Ser Leu Lys Asp Val Lys Ala Asn Ala Ser Asp Ser Lys Pro Ala  
 1 5 10 15  
 Gln Asp Lys Lys Asp Ala Lys Gln Gly Thr Glu Asp Ser Lys Asp Ser  
 20 25 30  
 Asp Lys Met Thr Glu Thr Asn Ser Val Pro Ala Gly Val Ile Val Val  
 35 40 45  
 Ser Leu Leu Ala Leu Leu Gly Val Ile Ala Phe Trp Leu Ile Arg Arg  
 50 55 60  
 Lys Lys Glu Ser Glu Ile Gln Gln Leu Ser Thr Glu Leu Ile Lys Val  
 65 70 75 80  
 Leu Gly Gln Leu Asp Ala Glu Lys Ala Asp Lys Lys Val Leu Ala Lys  
 85 90 95  
 Ala Gln Asn Leu Leu Gln Glu Thr Leu Asp Phe Val Lys Glu Glu Asn  
 100 105 110  
 Gly Ser Ala Glu Thr Glu Thr Lys Leu Val Glu Glu Leu Lys Ala Ile  
 115 120 125  
 Leu Asp Lys Leu Lys  
 130

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

09765272.012201

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

CAAGAAATCC TATCATCTCT TCCAGAAGCA AACAGAGACG AGGGGAATTC AGACTCAGTT 60  
 GATTGAAGAA TCGCTTAGTC AGCAGACTAT AATCCAGTCC TTCAATGCTC AAACAGAATT 120  
 TATCCAAAGA TTGCGTGAGG CTCATGACAA CTA CTAGGC TATTCTCAGT CAGCCATCTT 180  
 TTATTCTTCA ACGGTCAATC CTTGACTCG CTTTGTAAT GCACTCATTT ATGCCCTTTT 240  
 AGCTGGAGTA GGAGCTTATC GTATCATGAT GGGTTCAGCC TTGACCGTCG GTCGTTTAGT 300  
 GACTTTTTTG AACTATGTTC AGCAATACAC CAAGCCCTTT AACGATATTT CTTCAGTGCT 360  
 AGCTGAGTTG CAAAGTGCTC TGGCTTGCGT AGAGCGTATC TATGGAGTCT TAGATAGCCC 420  
 TGAAGTGGCT GAAACAGGTA AGGAAGTCTT GACGACCAGT GACCAAGTTA AGGGAGCTAT 480  
 TTCCTTTAAA CATGTCTCTT TTGGCTACCA TCCTGAAAAA ATTTTGATTA AGGACTTGTC 540  
 TATCGATATT CCAGCTGGTA GTAAGGTAGC CATCGTTGGT CCGACAGGTG CTGGAAAATC 600  
 AACTCTTATC AATCTCCTTA TGCCTTTTTT TCCATTAGC TCGGGAGATA TCTTGCTGGA 660  
 TGGGCAATCC ATTTATGATT ATACACGAGT ATCATTGAGA CAGCAGTTTG GTATGGTGCT 720  
 TCAAGAAACC TGGCTCACAC AAGGGACCAT TCATGATAAT ATTGCCTTTG GCAATCCTGA 780  
 AGCCAGTCGA GAGCAAGTAA TTGCTGCTGC CAAAGCAGCT AATGCAGACT TTTTCATCCA 840  
 ACAGTTGCCA CAGGGATACG ATACCAAGTT GGAAAATGCT GGAGAATCTC TCTCTGTCGG 900  
 CCAAGCTCAG CTCTTGACCA TAGCCCGAGT CTTTCTGGCT ATTCCAAAGA TTCTTATCTT 960  
 AGACGAGGCA ACTTCTTCCA TTGATACACG GACAGAAGTG CTGGTACAGG ATGCCTTTGC 1020  
 AAAACTCATG AAGGGCCGCA CAAGTTTCAT CATTGCTCAC CGTTTGTCOA CCATTCAGGA 1080  
 TCGGATTTA ATTCTTGCT TAGTAGATGG TGATATTGTT GAATATGGTA ACCATCAAGA 1140  
 ACTCATGGAT AGAAAGGGTA AGTATTACCA AATGCAAAAA GCTGCGGCTT TTAGTTCTGA 1200  
 A 1201

## (2) INFORMATION FOR SEQ ID NO:190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Lys Lys Ser Tyr His Leu Phe Gln Lys Gln Thr Glu Thr Arg Gly Ile  
 1 5 10 15  
 Gln Thr Gln Leu Ile Glu Glu Ser Leu Ser Gln Gln Thr Ile Ile Gln  
 20 25 30

09765272.012201

Ser Phe Asn Ala Gln Thr Glu Phe Ile Gln Arg Leu Arg Glu Ala His  
 35 40 45  
 Asp Asn Tyr Ser Gly Tyr Ser Gln Ser Ala Ile Phe Tyr Ser Ser Thr  
 50 55 60  
 Val Asn Pro Ser Thr Arg Phe Val Asn Ala Leu Ile Tyr Ala Leu Leu  
 65 70 75 80  
 Ala Gly Val Gly Ala Tyr Arg Ile Met Met Gly Ser Ala Leu Thr Val  
 85 90 95  
 Gly Arg Leu Val Thr Phe Leu Asn Tyr Val Gln Gln Tyr Thr Lys Pro  
 100 105 110  
 Phe Asn Asp Ile Ser Ser Val Leu Ala Glu Leu Gln Ser Ala Leu Ala  
 115 120 125  
 Cys Val Glu Arg Ile Tyr Gly Val Leu Asp Ser Pro Glu Val Ala Glu  
 130 135 140  
 Thr Gly Lys Glu Val Leu Thr Thr Ser Asp Gln Val Lys Gly Ala Ile  
 145 150 155 160  
 Ser Phe Lys His Val Ser Phe Gly Tyr His Pro Glu Lys Ile Leu Ile  
 165 170 175  
 Lys Asp Leu Ser Ile Asp Ile Pro Ala Gly Ser Lys Val Ala Ile Val  
 180 185 190  
 Gly Pro Thr Gly Ala Gly Lys Ser Thr Leu Ile Asn Leu Leu Met Arg  
 195 200 205  
 Phe Tyr Pro Ile Ser Ser Gly Asp Ile Leu Leu Asp Gly Gln Ser Ile  
 210 215 220  
 Tyr Asp Tyr Thr Arg Val Ser Leu Arg Gln Gln Phe Gly Met Val Leu  
 225 230 235 240  
 Gln Glu Thr Trp Leu Thr Gln Gly Thr Ile His Asp Asn Ile Ala Phe  
 245 250 255  
 Gly Asn Pro Glu Ala Ser Arg Glu Gln Val Ile Ala Ala Ala Lys Ala  
 260 265 270  
 Ala Asn Ala Asp Phe Phe Ile Gln Gln Leu Pro Gln Gly Tyr Asp Thr  
 275 280 285  
 Lys Leu Glu Asn Ala Gly Glu Ser Leu Ser Val Gly Gln Ala Gln Leu  
 290 295 300  
 Leu Thr Ile Ala Arg Val Phe Leu Ala Ile Pro Lys Ile Leu Ile Leu  
 305 310 315 320  
 Asp Glu Ala Thr Ser Ser Ile Asp Thr Arg Thr Glu Val Leu Val Gln  
 325 330 335  
 Asp Ala Phe Ala Lys Leu Met Lys Gly Arg Thr Ser Phe Ile Ile Ala  
 340 345 350  
 His Arg Leu Ser Thr Ile Gln Asp Ala Asp Leu Ile Leu Val Leu Val  
 355 360 365

00765272.012201

Asp Gly Asp Ile Val Glu Tyr Gly Asn His Gln Glu Leu Met Asp Arg  
 370 375 380

Lys Gly Lys Tyr Tyr Gln Met Gln Lys Ala Ala Ala Phe Ser Ser Glu  
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ACGAAATGCA GGGCAGACAG ATGCCTCGCA AATTGAAAAG GCGGCAGTTA GCCAAGGAGG 60  
 AAAAGCAGTG-AAAAAACAG AAATTAGTAA AGACGCAGAC TTGCACGAAA TTTATCTAGC 120  
 TGGAGGTTGT TTCTGGGGAG TGGAGGAATA TTTCTCACGT GTTCCCGGGG TGACGGATGC 180  
 CGTTTCAGGC TATGCAAATG GTAGAGGAGA AACAAACCAAG TACGAATTGA TTAACCAAAC 240  
 AGGTCATGCA GAAACCGTCC ATGTCACCTA TGATGCCAAG CAAATTTCTC TCAAGGAAAT 300  
 CCTGCTTCAC TATTTCCGCA TTATCAATCC AACCAGCAAA AATAACAAG GAAATGATGT 360  
 GGGGACCCAG TACCGTACTG GTGTTTATTA CACAGATGAC AAGGATTTGG AAGTGATTAA 420  
 CCAAGTCTTT GATGAGGTGG CTAAGAAATA CGATCAACCT CTAGCAGTTG AAAAGGAAAA 480  
 CTTGAAGAAT TTTGTGGTGG CTGAGGATTA CCATCAAGAC TATCTCAAGA AAAATCCAAA 540  
 TGGCTACTGC CATATCAATG TTAATCAGGC GGCCTATCCT GTCATTGATG CCAGCAAATA 600  
 TCCAAAACCA AGTGATGAGG AATTGAAAAA GACCCTGTCA CCTGAGGAGT ATGCAGTTAC 660  
 CCAGGAAAAT CAAACAGAAC GAGCTTTCTC AAACCGTTAC TGGGATAAAT TTGAATCCGG 720  
 TATCTATGTG GATATAGCAA CTGGGGAACC TCTCTTTTCA TCAAAGACA AATTGAGTC 780  
 TGGTTGTGGC TGGCCTAGTT TTACCCAACC CATCAGTCCA GATGTTGTCA CCTACAAGGA 840  
 AGATAAGTCC TACAATATGA CGCGTATGGA AGTGCGGAGC CGAGTAGGAG ATTCTCACCT 900  
 TGGGCATGTC TTTACGGATG GTCCACAGGA CAAGGGCGGC TTACGTTACT GTATCAATAG 960  
 CCTCTCTATC CGCTTTATTC CCAAAGACCA AATGGAAGAA AAAGGCTACG CTTATTTACT 1020  
 AGATTATGTT GAT 1033

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

09765072.012201

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Arg	Asn	Ala	Gly	Gln	Thr	Asp	Ala	Ser	Gln	Ile	Glu	Lys	Ala	Ala	Val	1	5	10	15
Ser	Gln	Gly	Gly	Lys	Ala	Val	Lys	Lys	Thr	Glu	Ile	Ser	Lys	Asp	Ala	20	25	30	
Asp	Leu	His	Glu	Ile	Tyr	Leu	Ala	Gly	Gly	Cys	Phe	Trp	Gly	Val	Glu	35	40	45	
Glu	Tyr	Phe	Ser	Arg	Val	Pro	Gly	Val	Thr	Asp	Ala	Val	Ser	Gly	Tyr	50	55	60	
Ala	Asn	Gly	Arg	Gly	Glu	Thr	Thr	Lys	Tyr	Glu	Leu	Ile	Asn	Gln	Thr	65	70	75	80
Gly	His	Ala	Glu	Thr	Val	His	Val	Thr	Tyr	Asp	Ala	Lys	Gln	Ile	Ser	85	90	95	
Leu	Lys	Glu	Ile	Leu	Leu	His	Tyr	Phe	Arg	Ile	Ile	Asn	Pro	Thr	Ser	100	105	110	
Lys	Asn	Lys	Gln	Gly	Asn	Asp	Val	Gly	Thr	Gln	Tyr	Arg	Thr	Gly	Val	115	120	125	
Tyr	Tyr	Thr	Asp	Asp	Lys	Asp	Leu	Glu	Val	Ile	Asn	Gln	Val	Phe	Asp	130	135	140	
Glu	Val	Ala	Lys	Lys	Tyr	Asp	Gln	Pro	Leu	Ala	Val	Glu	Lys	Glu	Asn	145	150	155	160
Leu	Lys	Asn	Phe	Val	Val	Ala	Glu	Asp	Tyr	His	Gln	Asp	Tyr	Leu	Lys	165	170	175	
Lys	Asn	Pro	Asn	Gly	Tyr	Cys	His	Ile	Asn	Val	Asn	Gln	Ala	Ala	Tyr	180	185	190	
Pro	Val	Ile	Asp	Ala	Ser	Lys	Tyr	Pro	Lys	Pro	Ser	Asp	Glu	Glu	Leu	195	200	205	
Lys	Lys	Thr	Leu	Ser	Pro	Glu	Glu	Tyr	Ala	Val	Thr	Gln	Glu	Asn	Gln	210	215	220	
Thr	Glu	Arg	Ala	Phe	Ser	Asn	Arg	Tyr	Trp	Asp	Lys	Phe	Glu	Ser	Gly	225	230	235	240
Ile	Tyr	Val	Asp	Ile	Ala	Thr	Gly	Glu	Pro	Leu	Phe	Ser	Ser	Lys	Asp	245	250	255	
Lys	Phe	Glu	Ser	Gly	Cys	Gly	Trp	Pro	Ser	Phe	Thr	Gln	Pro	Ile	Ser	260	265	270	
Pro	Asp	Val	Val	Thr	Tyr	Lys	Glu	Asp	Lys	Ser	Tyr	Asn	Met	Thr	Arg	275	280	285	
Met	Glu	Val	Arg	Ser	Arg	Val	Gly	Asp	Ser	His	Leu	Gly	His	Val	Phe	290	295	300	
Thr	Asp	Gly	Pro	Gln	Asp	Lys	Gly	Gly	Leu	Arg	Tyr	Cys	Ile	Asn	Ser	305	310	315	320

09765272.012201

Leu Ser Ile Arg Phe Ile Pro Lys Asp Gln Met Glu Glu Lys Gly Tyr  
 325 330 335

Ala Tyr Leu Leu Asp Tyr Val Asp  
 340

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

TGTATAGTTT	TTAGCGCTTG	TTCTTCTAAT	TCTGNTAAAA	ATGAAGAAAA	TACTTCTAAA	60
GAGCATGCGC	CTGATAAAAT	AGTTTTAGAT	CATGCTTTTCG	GTCAAACAT	ATTAGATAAA	120
AAACCTGAAA	GAGTTGCAAC	TATTGCTTGG	GGAAATCATG	ATGTAGCATT	AGCTTTAGGA	180
ATAGTTCCTG	TTGGATTTTC	AAAAGCAAAT	TACGGTGTA	GTGCTGATA	AGGAGTTT	240
CCATGGACAG	AAGAAAAAAT	CAAAGAACTA	AATGGTAAAG	CTAACCTATT	TGACGATTG	300
GATGGACTTA	ACTTTGAAGC	AATATCAAAT	TCTAAACCAG	ATGTTATCTT	AGCAGGTTAT	360
TCTGGTATAA	CTAAAGAAGA	TTATGACACT	CTATCA			396

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Cys	Ile	Val	Phe	Ser	Ala	Cys	Ser	Ser	Asn	Ser	Xaa	Lys	Asn	Glu	Glu
1				5					10					15	
Asn	Thr	Ser	Lys	Glu	His	Ala	Pro	Asp	Lys	Ile	Val	Leu	Asp	His	Ala
			20					25					30		
Phe	Gly	Gln	Thr	Ile	Leu	Asp	Lys	Lys	Pro	Glu	Arg	Val	Ala	Thr	Ile
		35					40				45				
Ala	Trp	Gly	Asn	His	Asp	Val	Ala	Leu	Ala	Leu	Gly	Ile	Val	Pro	Val
	50					55					60				
Gly	Phe	Ser	Lys	Ala	Asn	Tyr	Gly	Val	Ser	Ala	Asp	Lys	Gly	Val	Leu
65				70					75					80	
Pro	Trp	Thr	Glu	Glu	Lys	Ile	Lys	Glu	Leu	Asn	Gly	Lys	Ala	Asn	Leu
				85					90					95	

09765272.012201

Phe Asp Asp Leu Asp Gly Leu Asn Phe Glu Ala Ile Ser Asn Ser Lys  
 100 105 110

Pro Asp Val Ile Leu Ala Gly Tyr Ser Gly Ile Thr Lys Glu Asp Tyr  
 115 120 125

Asp Thr Leu Ser  
 130

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 844 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

GTGTGTCGAG CATATTCTGA AGCAAACCTA TCAAAATATA GAAATTATTT TAGTTGATGA	60
CGGTTCTACG GATAATTCTG GGGAAATTTG TGATGCTTTT ATGATGCAAG ATAATCGTGT	120
GCGAGTATTG CATCAAGAAA ATAAGGGGGG GGCAGCACAA GCTAAAAATA TGGGGATTAG	180
TGTAGCTAAG GGAGAGTACA TCACGATTGT TGATTCAGAT GATATCGTAA AAGAAAATAT	240
GATTGAAACT CTTTATCAGC AAGTCCAAGA AAAGGATGCA GATGTTGTTA TAGGGAATTA	300
CTATAATTAT GACGAAAGTG ACGGGAATTT TTATTTTAT GTAACAGGGC AAGATTTTGT	360
CGTCGAAGAA TTAGCTATAC AAGAAATTAT GAACCGTCAA GCAGGAGATT GGAAATTCAA	420
TAGCTCGGCC TTTATATTGC CGACATTTAA GTTGATTAAA AAAGAATTAT TCAATGAAGT	480
TCACTTTTCA AATGGTGCCT GCTTTGATGA TGAAGCAACT ATGCATCGCT TTTATCTTTT	540
AGCCTCTAAA ATCGTCTTTA TAAACGATAA TCTCTATCTG TATAGAAGAC GTTCAGGAAG	600
CATCATGAGA ACGGAATTTG ATCTTTCCTG GGCAAGAGAT ATTGTTGAAG TGTTTTCTAA	660
GAAAATATCG GATTGTGTCT TGGCTGGTTT GGATGTCTCC GTTCTGCGTA TTCGATTGT	720
CAATCTTTTA AAAGATTATA AGCAAACCTT AGAATACCAT CAATTAACAG ATACTGAGGA	780
ATATAAAGAT ATTTGTTTCA GATTAAAGTT GTTTTTTGAT GCAGAACAAA GAAATGGTAA	840
AAGT	844

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 281 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

09765272.012201



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Cys Val Glu His Ile Leu Lys Gln Thr Tyr Gln Asn Ile Glu Ile Ile  
 1 5 10 15  
 Leu Val Asp Asp Gly Ser Thr Asp Asn Ser Gly Glu Ile Cys Asp Ala  
 20 25 30  
 Phe Met Met Gln Asp Asn Arg Val Arg Val Leu His Gln Glu Asn Lys  
 35 40 45  
 Gly Gly Ala Ala Gln Ala Lys Asn Met Gly Ile Ser Val Ala Lys Gly  
 50 55 60  
 Glu Tyr Ile Thr Ile Val Asp Ser Asp Asp Ile Val Lys Glu Asn Met  
 65 70 75 80  
 Ile Glu Thr Leu Tyr Gln Gln Val Gln Glu Lys Asp Ala Asp Val Val  
 85 90 95  
 Ile Gly Asn Tyr Tyr Asn Tyr Asp Glu Ser Asp Gly Asn Phe Tyr Phe  
 100 105 110  
 Tyr Val Thr Gly Gln Asp Phe Cys Val Glu Glu Leu Ala Ile Gln Glu  
 115 120 125  
 Ile Met Asn Arg Gln Ala Gly Asp Trp Lys Phe Asn Ser Ser Ala Phe  
 130 135 140  
 Ile Leu Pro Thr Phe Lys Leu Ile Lys Lys Glu Leu Phe Asn Glu Val  
 145 150 155 160  
 His Phe Ser Asn Gly Arg Arg Phe Asp Asp Glu Ala Thr Met His Arg  
 165 170 175  
 Phe Tyr Leu Leu Ala Ser Lys Ile Val Phe Ile Asn Asp Asn Leu Tyr  
 180 185 190  
 Leu Tyr Arg Arg Arg Ser Gly Ser Ile Met Arg Thr Glu Phe Asp Leu  
 195 200 205  
 Ser Trp Ala Arg Asp Ile Val Glu Val Phe Ser Lys Lys Ile Ser Asp  
 210 215 220  
 Cys Val Leu Ala Gly Leu Asp Val Ser Val Leu Arg Ile Arg Phe Val  
 225 230 235 240  
 Asn Leu Leu Lys Asp Tyr Lys Gln Thr Leu Glu Tyr His Gln Leu Thr  
 245 250 255  
 Asp Thr Glu Glu Tyr Lys Asp Ile Cys Phe Arg Leu Lys Leu Phe Phe  
 260 265 270  
 Asp Ala Glu Gln Arg Asn Gly Lys Ser  
 275 280

## (2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 811 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

0975272.012201

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GTGTTTGGAT AGCATTTCAGA ATCAGACGTA TCAAAATTTT GAGTGTTTAT TAATCAATGA 60  
 TGGCTCTCCA GATCATTTCAT CCAAAATATG TGAAGAATTT GTAGAGAAAG ATTCTCGTTT 120  
 CAAATATTTT GAGAAAGCAA ACGGCGGTCT TTCATCAGCT CGTAACCTAG GTATTGAATG 180  
 TTCGGGGGGG GCGTACATTA CTTTTGTAGA CTCTGATGAT TGGTTGGAAC ATGATGCTTT 240  
 AGACCGATTA TATGGTGCTT TGAAAAAGGA AAACGCAGAT ATTAGTATCG GCGTTATAA 300  
 TTCTTATGAT GAAACACGCT ATGTGTATAT GACTTATGTT ACGGATCCAG ATGATTCTCT 360  
 AGAAGTGATA GAAGGTAAAG CAATTATGGA TAGGGAAGGT GTCGAAGAAG TCAGAAATGG 420  
 GAACTGGACT GTAGCTGTCT TGAAGTTATT CAAGAGAGAG TTACTACAAG ATTTACCATT 480  
 TCCTATAGGA AAAATTGCAG AGGATACTTA CTGGACATGG AAGGTACTTC TAAGAGCTTC 540  
 GAGGATAGTC TATTTGAATC GTTGTGTTTA CTGGTACCGT GTTGGTTTAT CTGATACTTT 600  
 ATCGAATACA TGGAGTGAAA AGCGTATGTA TGATGAAATT GGGGCTAGGG AAGAAAAGAT 660  
 AGCTATTTTA GCAAGTTCAG ACTATGACTT GACCAATCAT ATTTTGATTT ATAAAAATAG 720  
 ATTACAAAGA GTGATAGCAA AATTAGAAGA ACAAATATG CAGTTCACAG AGATTTCACAG 780  
 AAGAATGATG GAAAAATTGT CTTTACTTCC G 811

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Cys Leu Asp Ser Ile Gln Asn Gln Thr Tyr Gln Asn Phe Glu Cys Leu  
 1 5 10 15  
 Leu Ile Asn Asp Gly Ser Pro Asp His Ser Ser Lys Ile Cys Glu Glu  
 20 25 30  
 Phe Val Glu Lys Asp Ser Arg Phe Lys Tyr Phe Glu Lys Ala Asn Gly  
 35 40 45  
 Gly Leu Ser Ser Ala Arg Asn Leu Gly Ile Glu Cys Ser Gly Gly Ala  
 50 55 60  
 Tyr Ile Thr Phe Val Asp Ser Asp Asp Trp Leu Glu His Asp Ala Leu  
 65 70 75 80  
 Asp Arg Leu Tyr Gly Ala Leu Lys Lys Glu Asn Ala Asp Ile Ser Ile  
 85 90 95

09765272.012201

Gly Arg Tyr Asn Ser Tyr Asp Glu Thr Arg Tyr Val Tyr Met Thr Tyr  
 100 105 110  
 Val Thr Asp Pro Asp Asp Ser Leu Glu Val Ile Glu Gly Lys Ala Ile  
 115 120 125  
 Met Asp Arg Glu Gly Val Glu Glu Val Arg Asn Gly Asn Trp Thr Val  
 130 135 140  
 Ala Val Leu Lys Leu Phe Lys Arg Glu Leu Leu Gln Asp Leu Pro Phe  
 145 150 155 160  
 Pro Ile Gly Lys Ile Ala Glu Asp Thr Tyr Trp Thr Trp Lys Val Leu  
 165 170 175  
 Leu Arg Ala Ser Arg Ile Val Tyr Leu Asn Arg Cys Val Tyr Trp Tyr  
 180 185 190  
 Arg Val Gly Leu Ser Asp Thr Leu Ser Asn Thr Trp Ser Glu Lys Arg  
 195 200 205  
 Met Tyr Asp Glu Ile Gly Ala Arg Glu Glu Lys Ile Ala Ile Leu Ala  
 210 215 220  
 Ser Ser Asp Tyr Asp Leu Thr Asn His Ile Leu Ile Tyr Lys Asn Arg  
 225 230 235 240  
 Leu Gln Arg Val Ile Ala Lys Leu Glu Glu Gln Asn Met Gln Phe Thr  
 245 250 255  
 Glu Ile Tyr Arg Arg Met Met Glu Lys Leu Ser Leu Leu Pro  
 260 265 270

## (2) INFORMATION FOR SEQ ID NO: 199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGCCTAGAT AGTATTATTA CTCAAACATA TAAAAATATT GAGATTGTTG TCGTTAATGA	60
TGGTTCTACG GATGCTTCAG GTGAAATTTG TAAAGAATTT TCAGAAATGG ATCACCGAAT	120
TCTCTATATA GAACAAGAAA ATGCTGGTCT TTCTGCCGCA CGAAACACCG GTCTGAATAA	180
TATGTCCGGA AATTATGTGA CCTTTGTGGA CTCGGATGAT TGGATTGAGC AAGATTATGT	240
AGAAACTCTA TATAAAAAA TAGTAGAGTA TCAGGCTGAT ATTGCAGTTG GTAATTATTA	300
TTCTTTCAAC GAAAGTGAAG GAATGTTCTA CTTTCATATA TTGGGAGACT CCTATTATGA	360
GAAAGTATAT GATAATGTTT CTATCTTTGA GAACTTGAT GAAACTCAAG AAATGAAGAG	420
TTTTGCTTTG ATATCTGCTT GGGGTAACT CTATAAGGCA AGATTGTTTG AGCAGTTGCG	480
CTTTGACATA GGTAATTAG GAGAAGATGG TTACCTCAAT CAAAAGGTAT ATTTATTATC	540

00765272.012201

AGAAAAGGTA ATTTATTTAA ATAAAAGTCT TTATGCTTAT CGGATTAGAA AAGGTAGTTT 600  
 ATCAAGAGTT TGGACAGAAA AGTGGATGCA CGCTTTAGTT GATGCTATGT CTGAACGTAT 660  
 TACGCTACTA GCTAATATGG GTTATCCTCT AGAGAAACAC TTGGCAGTTT ATCGTCAGAT 720  
 GTTGGAAGTC AGTCTCGCCA ACGGTCAAGC TAGTGGTTTA TCTGACACAG CAACGTATAA 780  
 AGAGTTTGAA ATGAAACAAA GGCTTTTAAA TCAGCTATCG AGACAAGAGG AAAGTGAAAA 840  
 GAAAGCCATT GTCCTCGCAG CAACTATGG CTATGTAGAC CAAGTTTTAA CGACAATCAA 900  
 GTCTATTTGT TATCATAATC GTTCGATTCG TTTTATCTG ATTCATAGCG ATTTTCCAAA 960  
 TGAATGGATT AAGCAATTAA ATAAGCGCTT AGAGAAGTTT GACTCAGAAA TTATTAATTG 1020  
 TCGGGTAACT TCTGAGCAAA TTTCATGTTA TAAATCGGAT ATTAGTTACA CAGTCTTTTT 1080  
 ACGCTATTTT ATAGCTGATT TCGTGCAAGA AGACAAGGCC CTCTACTTGG ACTGTGATCT 1140  
 AGTTGTAACG AAAAATCTGG ATGACTTGTT TGCTACAGAC TTACAAGATT ATCCTTTGGC 1200  
 TGCTGTTAGA GATTTTGGGG GCAGAGCTTA TTTTGGTCAA GAAATCTTTA ATGCCGGTGT 1260  
 TCTCTTGGA AACAATGCTT TTTGAAAAA AGAGAATATG ACCCAAAAAT TAATTGATGT 1320  
 Aaccaatgaa TGGCATGATA AGGTGGATCA GGCAGATCAG AGCATCTTGA ATATGCTTTT 1380  
 TGAACATAAA TGGTTGGAAT TGGACTTTGA TTATAATCAT ATTGTCATTC ATAAACAGTT 1440  
 TGCTGATTAT CAATTGCCTG AGGGTCAGGA TTATCCTGCT ATTATTCATC ATCTTTCTCA 1500  
 TCGGAAACCG TGGAAAGATT TGGCGGCCCA AACCTATCGT GAAGTTTGGT GGTACTATCA 1560  
 TGGGCTTGAA TGGACAGAAT TGGGACAAAA CCATCATTTA CATCCATTAC AAAGATCTCA 1620  
 CATCTATCCA ATAAAGGAAC CTTTCACTTG TCTAATCTAT ACTGCCTCAG ACCATATTGA 1680  
 ACAAATTGAG ACATTGGTTC AATCCTTGCC TGATATTCAG TTTAAGATAG CAGCTAGAGT 1740  
 AATAGTTAGT GATCGATTGG CTCAGATGAC AATTTATCCA AACGTGACTA TATTTAACGG 1800  
 AATTCATCTAT TTGGTAGATG TCGATAATGA ATTGGTAGAA ACCAGTCAAG TACTTTTAGA 1860  
 TATTAATCAT GGCGAAAAGA CAGAAGAAAT TCTCGATCAA TTTGCTAATC TTGGCAAGCC 1920  
 TATCTTATCC TTTGAAAATA CTAAACCTA TGAAGTAGGT CAGGAGGCAT ATGCTGTTGA 1980  
 CCAAGTTCAA GCAATGATTG AAAAATTGAG AGAAATAAGC AAA 2023

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

097655272.012201

Cys Leu Asp Ser Ile Ile Thr Gln Thr Tyr Lys Asn Ile Glu Ile Val  
 1 5 10 15  
 Val Val Asn Asp Gly Ser Thr Asp Ala Ser Gly Glu Ile Cys Lys Glu  
 20 25 30  
 Phe Ser Glu Met Asp His Arg Ile Leu Tyr Ile Glu Gln Glu Asn Ala  
 35 40 45  
 Gly Leu Ser Ala Ala Arg Asn Thr Gly Leu Asn Asn Met Ser Gly Asn  
 50 55 60  
 Tyr Val Thr Phe Val Asp Ser Asp Asp Trp Ile Glu Gln Asp Tyr Val  
 65 70 75 80  
 Glu Thr Leu Tyr Lys Lys Ile Val Glu Tyr Gln Ala Asp Ile Ala Val  
 85 90 95  
 Gly Asn Tyr Tyr Ser Phe Asn Glu Ser Glu Gly Met Phe Tyr Phe His  
 100 105 110  
 Ile Leu Gly Asp Ser Tyr Tyr Glu Lys Val Tyr Asp Asn Val Ser Ile  
 115 120 125  
 Phe Glu Asn Leu Tyr Glu Thr Gln Glu Met Lys Ser Phe Ala Leu Ile  
 130 135 140  
 Ser Ala Trp Gly Lys Leu Tyr Lys Ala Arg Leu Phe Glu Gln Leu Arg  
 145 150 155 160  
 Phe Asp Ile Gly Lys Leu Gly Glu Asp Gly Tyr Leu Asn Gln Lys Val  
 165 170 175  
 Tyr Leu Leu Ser Glu Lys Val Ile Tyr Leu Asn Lys Ser Leu Tyr Ala  
 180 185 190  
 Tyr Arg Ile Arg Lys Gly Ser Leu Ser Arg Val Trp Thr Glu Lys Trp  
 195 200 205  
 Met His Ala Leu Val Asp Ala Met Ser Glu Arg Ile Thr Leu Leu Ala  
 210 215 220  
 Asn Met Gly Tyr Pro Leu Glu Lys His Leu Ala Val Tyr Arg Gln Met  
 225 230 235 240  
 Leu Glu Val Ser Leu Ala Asn Gly Gln Ala Ser Gly Leu Ser Asp Thr  
 245 250 255  
 Ala Thr Tyr Lys Glu Phe Glu Met Lys Gln Arg Leu Leu Asn Gln Leu  
 260 265 270  
 Ser Arg Gln Glu Glu Ser Glu Lys Lys Ala Ile Val Leu Ala Ala Asn  
 275 280 285  
 Tyr Gly Tyr Val Asp Gln Val Leu Thr Thr Ile Lys Ser Ile Cys Tyr  
 290 295 300  
 His Asn Arg Ser Ile Arg Phe Tyr Leu Ile His Ser Asp Phe Pro Asn  
 305 310 315 320  
 Glu Trp Ile Lys Gln Leu Asn Lys Arg Leu Glu Lys Phe Asp Ser Glu  
 325 330 335

09765272.012201

Ile Ile Asn Cys Arg Val Thr Ser Glu Gln Ile Ser Cys Tyr Lys Ser  
 340 345 350  
 Asp Ile Ser Tyr Thr Val Phe Leu Arg Tyr Phe Ile Ala Asp Phe Val  
 355 360 365  
 Gln Glu Asp Lys Ala Leu Tyr Leu Asp Cys Asp Leu Val Val Thr Lys  
 370 375 380  
 Asn Leu Asp Asp Leu Phe Ala Thr Asp Leu Gln Asp Tyr Pro Leu Ala  
 385 390 395 400  
 Ala Val Arg Asp Phe Gly Gly Arg Ala Tyr Phe Gly Gln Glu Ile Phe  
 405 410 415  
 Asn Ala Gly Val Leu Leu Val Asn Asn Ala Phe Trp Lys Lys Glu Asn  
 420 425 430  
 Met Thr Gln Lys Leu Ile Asp Val Thr Asn Glu Trp His Asp Lys Val  
 435 440 445  
 Asp Gln Ala Asp Gln Ser Ile Leu Asn Met Leu Phe Glu His Lys Trp  
 450 455 460  
 Leu Glu Leu Asp Phe Asp Tyr Asn His Ile Val Ile His Lys Gln Phe  
 465 470 475 480  
 Ala Asp Tyr Gln Leu Pro Glu Gly Gln Asp Tyr Pro Ala Ile Ile His  
 485 490 495  
 Tyr Leu Ser His Arg Lys Pro Trp Lys Asp Leu Ala Ala Gln Thr Tyr  
 500 505 510  
 Arg Glu Val Trp Trp Tyr Tyr His Gly Leu Glu Trp Thr Glu Leu Gly  
 515 520 525  
 Gln Asn His His Leu His Pro Leu Gln Arg Ser His Ile Tyr Pro Ile  
 530 535 540  
 Lys Glu Pro Phe Thr Cys Leu Ile Tyr Thr Ala Ser Asp His Ile Glu  
 545 550 555 560  
 Gln Ile Glu Thr Leu Val Gln Ser Leu Pro Asp Ile Gln Phe Lys Ile  
 565 570 575  
 Ala Ala Arg Val Ile Val Ser Asp Arg Leu Ala Gln Met Thr Ile Tyr  
 580 585 590  
 Pro Asn Val Thr Ile Phe Asn Gly Ile His Tyr Leu Val Asp Val Asp  
 595 600 605  
 Asn Glu Leu Val Glu Thr Ser Gln Val Leu Leu Asp Ile Asn His Gly  
 610 615 620  
 Glu Lys Thr Glu Glu Ile Leu Asp Gln Phe Ala Asn Leu Gly Lys Pro  
 625 630 635 640  
 Ile Leu Ser Phe Glu Asn Thr Lys Thr Tyr Glu Val Gly Gln Glu Ala  
 645 650 655  
 Tyr Ala Val Asp Gln Val Gln Ala Met Ile Glu Lys Leu Arg Glu Ile  
 660 665 670

09765272.012201

Ser Lys

## (2) INFORMATION FOR SEQ ID NO: 201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

CATTGAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT GTTGATGATG GTGCAACAGA 60  
 TGAAAGTGGT CGCTTGTGTG ATTCAATCGC TGAACAAGAT GACAGGGTGT CAGTGCTTCA 120  
 TAAAAAGAAC GAAGGATTGT CGCAAGCAGC AAATGATGGG ATGAAGCAGG CTCACGGGGA 180  
 TTATCTGATT TTTATTGACT CAGATGATTA TATCCATCCA GAAATGATTC AGAGCTTATA 240  
 TGAGCAATTA GTTCAAGAAG ATGCGGATGT TTCGAGCTGT GGTGTCATGA ATGTCTATGC 300  
 TAATGATGAA AGCCACAGT CAGCCAATCA GGATGACTAT TTTGTCTGTG ATTCTCAAAC 360  
 ATTTCTAAAG GAATACCTCA TAGGTGAAAA AATACCTGGG ACGATTTGCA ATAAGCTAAT 420  
 CAAGAGACAG ATTGCAACTG CCCTATCCTT TCCTAAGGGG TTGATTTACG AAGATGCCTA 480  
 TTACCATTTT GATTTAATCA AGTTGGCCAA GAAGTATGTG GTTAATACTA AACCCTATTA 540  
 TTACTATTTT CATAGAGGGG ATAGTATTAC GACCAAACCC TATGCAGAGA AGGATTTAGC 600  
 CTATATTGAT ATCTACCAA AGTTTTATAA TGAAGTTGTG AAAAATATC CTGACTTGAA 660  
 AGAGGTCGCT TTTTTCAGAT TGGCCTATGC CCACTTCTTT ATTCTGGATA AGATGTTGCT 720  
 AGATGATCAG TATAACAGT TTGAAGCCTA TTCTCAGATT CATCGTTTTT TAAAAGGCCA 780  
 TGCCTTTGCT ATTTCTAGGA ATCCAATTTT CCGTAAGGGG AGAAGAATTA GTGCTTTGGC 840  
 CCTATTCATA AATATTCCT TATATCGATT CTTATTACTG AAAAATATTG AAAAATCTAA 900  
 AAAATTACAT 910

## (2) INFORMATION FOR SEQ ID NO:202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Ile Gln Lys Gln Thr Tyr Gln Asn Leu Glu Ile Ile Leu Val Asp Asp  
 1 5 10 15

09765272.012204

Gly Ala Thr Asp Glu Ser Gly Arg Leu Cys Asp Ser Ile Ala Glu Gln  
 20 25 30  
 Asp Asp Arg Val Ser Val Leu His Lys Lys Asn Glu Gly Leu Ser Gln  
 35 40 45  
 Ala Arg Asn Asp Gly Met Lys Gln Ala His Gly Asp Tyr Leu Ile Phe  
 50 55 60  
 Ile Asp Ser Asp Asp Tyr Ile His Pro Glu Met Ile Gln Ser Leu Tyr  
 65 70 75 80  
 Glu Gln Leu Val Gln Glu Asp Ala Asp Val Ser Ser Cys Gly Val Met  
 85 90 95  
 Asn Val Tyr Ala Asn Asp Glu Ser Pro Gln Ser Ala Asn Gln Asp Asp  
 100 105 110  
 Tyr Phe Val Cys Asp Ser Gln Thr Phe Leu Lys Glu Tyr Leu Ile Gly  
 115 120 125  
 Glu Lys Ile Pro Gly Thr Ile Cys Asn Lys Leu Ile Lys Arg Gln Ile  
 130 135 140  
 Ala Thr Ala Leu Ser Phe Pro Lys Gly Leu Ile Tyr Glu Asp Ala Tyr  
 145 150 155 160  
 Tyr His Phe Asp Leu Ile Lys Leu Ala Lys Lys Tyr Val Val Asn Thr  
 165 170 175  
 Lys Pro Tyr Tyr Tyr Tyr Phe His Arg Gly Asp Ser Ile Thr Thr Lys  
 180 185 190  
 Pro Tyr Ala Glu Lys Asp Leu Ala Tyr Ile Asp Ile Tyr Gln Lys Phe  
 195 200 205  
 Tyr Asn Glu Val Val Lys Asn Tyr Pro Asp Leu Lys Glu Val Ala Phe  
 210 215 220  
 Phe Arg Leu Ala Tyr Ala His Phe Phe Ile Leu Asp Lys Met Leu Leu  
 225 230 235 240  
 Asp Asp Gln Tyr Lys Gln Phe Glu Ala Tyr Ser Gln Ile His Arg Phe  
 245 250 255  
 Leu Lys Gly His Ala Phe Ala Ile Ser Arg Asn Pro Ile Phe Arg Lys  
 260 265 270  
 Gly Arg Arg Ile Ser Ala Leu Ala Leu Phe Ile Asn Ile Ser Leu Tyr  
 275 280 285  
 Arg Phe Leu Leu Leu Lys Asn Ile Glu Lys Ser Lys Lys Leu His  
 290 295 300

## (2) INFORMATION FOR SEQ ID NO: 203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

00765272.0122001



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

TAAGGCTGAT AATCGTGTTT AAATGAGAAC GACGATTAAT AATGAATCGC CATTGTTGCT	60
TTCTCCGTTG TATGGCAATG ATAATGGTAA CGGATTATGG TGGGGGAACA CATTGAAGGG	120
AGCATGGGAA GCTATTCCTG AAGATGTAAA GCCATATGCA GCGATTGAAC TTCATCCTGC	180
AAAAGTCTGT AAACCAACAA GTTGTATTCC ACGAGATACG AAAGAATTGA GAGAATGGTA	240
TGTCAAGATG TTGGAGGAAG CTCAAAGTCT AAACATTCCA GTTTTCTTGG TTATTATGTC	300
GGCTGGAGAG CGTAATACAG TTCCTCCAGA GTGGTTAGAT GAACAATTCC AAAAGTATAG	360
TGTGTTAAAA GGTGTTTTAA ATATTGAGAA TTATTGGATT TACAATAACC AGTTAGCTCC	420
GCATAGTGCT AAATATTTGG AAGTTTGTGC CAAATATGGA GCGCATTTTA TCTGGCATGA	480
TCATGAAAAA TGGTTCTGGG AAACATTAT GAATGATCCG ACATTCTTTG AAGCGAGTCA	540
AAAATATCAT AAAAATTTGG TGTGGCAAC TAAAAATACG CCAATAAGAG ATGATGCGGG	600
TACAGATTCT ATCGTTAGTG GATTTTGGTT GAGTGGCTTA TGTGATAACT GGGGCTCATC	660
AACAGATACA TGGAAATGGT GGGAAAAACA TTATACAAAC ACATTTGAAA CTGGAAGAGC	720
TAGGGATATG AGATCCTATG CATCGGAACC AGAATCAATG ATTGCTATGG AAATGATGAA	780
TGTATATACT GGGGGAGGCA CAGTTTATAA TTTCGAATGT GCCGCGTATA CATTTATGAC	840
AAATGATGTA CCAACTCCAG CATTTACTAA AGGTATTATT CCTTTCTTTA GACATGCTAT	900
ACAAAATCCA GCTCCAAGTA AGGAAGAAGT TGTAATAGA ACAAAGCTG TATTTTGGAA	960
TGGAGAAGGT AGGATTAGTT CATTAAACGG ATTTTATCAA GGACTTTATT CGAATGATGA	1020
AACAATGCCT TTATATAATA ATGGGAGATA TCATATTCTT CCTGTAATAC ATGAGAAAAT	1080
TGATAAGGAA AAGATTTTAT CTATATTCCC TAATGCAAAA ATTTTACTA AAAATAGTGA	1140
GGAATTGTCT AGTAAAGTCA ACTATTTAAA CTCGCTTTAT CCAAACTTT ATGAAGGAGA	1200
TGGGTATGCT CAGCGTGTAG GTAATTCCTG GTATATTTAT AATAGTAATG CTAATATCAA	1260
TAAAAATCAG CAAGTAATGT TGCCTATGTA TACTAATAAT ACAAAGTCGT TATCGTTAGA	1320
TTTGACGCCA CATACTTACG CTGTTGTTAA AGAAAATCCA AATAATTTAC ATATTTTATT	1380
GAATAATTAC AGGACAGATA AGACAGCTAT GTGGGCATTA TCAGGAAATT TTGATGCATC	1440
AAAAAGTTGG AAGAAAGAAG AATTAGAGTT AGCGAACTGG ATAAGCAAAA ATTATTCCAT	1500
CAATCCTGTA GATAATGACT TTAGGACAAC AACACTTACA TTAAAGGGC ATACTGGTCA	1560
TAAACCTCAG ATAAATATAA GTGGCGATAA AAATCATTAT ACTTATACAG AAAATTGGGA	1620
TGAGAATACC CATGTTTATA CCATTACGGT TAATCATAAT GGAATGGTAG AGATGTCTAT	1680
AAATACTGAG GGGACAGGTC CAGTCTCTTT CCCAACACCA GATAAATTTA ATGATGGTAA	1740
TTTGAATATA GCATATGCAA AACCAACAAC ACAAAGTTCT GTAGATTACA ATGGAGACCC	1800

TAATAGAGCT GTGGATGGTA ACAGAAATGG TAATTTTAAC TCTGGTTCGG TAACACACAC 1860  
 TAGGGCAGAT AATCCCTCTT GGTGGGAAGT CGATTTGAAA AAAATGGATA AAGTTGGGCT 1920  
 TGTAAAAATT TATAATCGCA CAGATGCTGA GACTCAACGT CTATCTAATT TT 1972

## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Lys Ala Asp Asn Arg Val Gln Met Arg Thr Thr Ile Asn Asn Glu Ser  
 1 5 10 15  
 Pro Leu Leu Leu Ser Pro Leu Tyr Gly Asn Asp Asn Gly Asn Gly Leu  
 20 25 30  
 Trp Trp Gly Asn Thr Leu Lys Gly Ala Trp Glu Ala Ile Pro Glu Asp  
 35 40 45  
 Val Lys Pro Tyr Ala Ala Ile Glu Leu His Pro Ala Lys Val Cys Lys  
 50 55 60  
 Pro Thr Ser Cys Ile Pro Arg Asp Thr Lys Glu Leu Arg Glu Trp Tyr  
 65 70 75 80  
 Val Lys Met Leu Glu Ala Gln Ser Leu Asn Ile Pro Val Phe Leu  
 85 90 95  
 Val Ile Met Ser Ala Gly Glu Arg Asn Thr Val Pro Pro Glu Trp Leu  
 100 105 110  
 Asp Glu Gln Phe Gln Lys Tyr Ser Val Leu Lys Gly Val Leu Asn Ile  
 115 120 125  
 Glu Asn Tyr Trp Ile Tyr Asn Asn Gln Leu Ala Pro His Ser Ala Lys  
 130 135 140  
 Tyr Leu Glu Val Cys Ala Lys Tyr Gly Ala His Phe Ile Trp His Asp  
 145 150 155 160  
 His Glu Lys Trp Phe Trp Glu Thr Ile Met Asn Asp Pro Thr Phe Phe  
 165 170 175  
 Glu Ala Ser Gln Lys Tyr His Lys Asn Leu Val Leu Ala Thr Lys Asn  
 180 185 190  
 Thr Pro Ile Arg Asp Asp Ala Gly Thr Asp Ser Ile Val Ser Gly Phe  
 195 200 205  
 Trp Leu Ser Gly Leu Cys Asp Asn Trp Gly Ser Ser Thr Asp Thr Trp  
 210 215 220  
 Lys Trp Trp Glu Lys His Tyr Thr Asn Thr Phe Glu Thr Gly Arg Ala

F022F0"2259760

225		230		235		240
Arg Asp Met Arg Ser Tyr Ala Ser Glu Pro Glu Ser Met Ile Ala Met						
		245		250		255
Glu Met Met Asn Val Tyr Thr Gly Gly Gly Thr Val Tyr Asn Phe Glu		260		265		270
Cys Ala Ala Tyr Thr Phe Met Thr Asn Asp Val Pro Thr Pro Ala Phe		275		280		285
Thr Lys Gly Ile Ile Pro Phe Phe Arg His Ala Ile Gln Asn Pro Ala		290		295		300
Pro Ser Lys Glu Glu Val Val Asn Arg Thr Lys Ala Val Phe Trp Asn		305		310		315
Gly Glu Gly Arg Ile Ser Ser Leu Asn Gly Phe Tyr Gln Gly Leu Tyr		325		330		335
Ser Asn Asp Glu Thr Met Pro Leu Tyr Asn Asn Gly Arg Tyr His Ile		340		345		350
Leu Pro Val Ile His Glu Lys Ile Asp Lys Glu Lys Ile Ser Ser Ile		355		360		365
Phe Pro Asn Ala Lys Ile Leu Thr Lys Asn Ser Glu Glu Leu Ser Ser		370		375		380
Lys Val Asn Tyr Leu Asn Ser Leu Tyr Pro Lys Leu Tyr Glu Gly Asp		385		390		395
Gly Tyr Ala Gln Arg Val Gly Asn Ser Trp Tyr Ile Tyr Asn Ser Asn		405		410		415
Ala Asn Ile Asn Lys Asn Gln Gln Val Met Leu Pro Met Tyr Thr Asn		420		425		430
Asn Thr Lys Ser Leu Ser Leu Asp Leu Thr Pro His Thr Tyr Ala Val		435		440		445
Val Lys Glu Asn Pro Asn Asn Leu His Ile Leu Leu Asn Asn Tyr Arg		450		455		460
Thr Asp Lys Thr Ala Met Trp Ala Leu Ser Gly Asn Phe Asp Ala Ser		465		470		475
Lys Ser Trp Lys Lys Glu Glu Leu Glu Leu Ala Asn Trp Ile Ser Lys		485		490		495
Asn Tyr Ser Ile Asn Pro Val Asp Asn Asp Phe Arg Thr Thr Thr Leu		500		505		510
Thr Leu Lys Gly His Thr Gly His Lys Pro Gln Ile Asn Ile Ser Gly		515		520		525
Asp Lys Asn His Tyr Thr Tyr Thr Glu Asn Trp Asp Glu Asn Thr His		530		535		540
Val Tyr Thr Ile Thr Val Asn His Asn Gly Met Val Glu Met Ser Ile		545		550		555
Asn Thr Glu Gly Thr Gly Pro Val Ser Phe Pro Thr Pro Asp Lys Phe						560

09765272-012201

565 570 575  
 Asn Asp Gly Asn Leu Asn Ile Ala Tyr Ala Lys Pro Thr Thr Gln Ser  
 580 585 590  
 Ser Val Asp Tyr Asn Gly Asp Pro Asn Arg Ala Val Asp Gly Asn Arg  
 595 600 605  
 Asn Gly Asn Phe Asn Ser Gly Ser Val Thr His Thr Arg Ala Asp Asn  
 610 615 620  
 Pro Ser Trp Trp Glu Val Asp Leu Lys Lys Met Asp Lys Val Gly Leu  
 625 630 635 640  
 Val Lys Ile Tyr Asn Arg Thr Asp Ala Glu Thr Gln Arg Leu Ser Asn  
 645 650 655  
 Phe

## (2) INFORMATION FOR SEQ ID NO: 205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

CTGTGGCAAT CAGTCAGCTG CTTCCAAACA GTCAGCTTCA GGAACGATTG AGGTGATTTC	60
ACGAGAAAAT GGCTCTGGGA CACGGGGTGC CTTACAGAA ATCACAGGGA TTCTCAAAAA	120
AGACGGTGAT AAAAAAATTG ACAACACTGC CAAAACAGCT GTGATTCAAA ATAGTACAGA	180
AGGTGTTCTC TCAGCAGTTC AAGGGAATGC TAATGCTATC GGCTACATCT CCTTGGGATC	240
TTTAACGAAA TCTGTCAAGG CTTTAGAGAT TGATGGTGTC AAGGCTAGTC GAGACACAGT	300
TTTAGATGGT GAATACCCTC TTCAACGTCC CTTCAACATT GTTTGGTCTT CTAATCTTTC	360
CAAGCTAGGT CAAGATTTTA TCAGCTTTAT CCACTCCAAA CAAGGTCAAC AAGTGGTCAC	420
AGATAATAAA TTTATTGAAG CTAAAACCGA AACCACGGAA TATACAAGCC AACACTTATC	480
AGGCAAGTTG TCTGTTGTAG GTTCCACTTC AGTATCTTCT TTAATGGAAA AATTAGCAGA	540
AGCTTATAAA AAAGAAAATC CAGAAGTTAC GATTGATATT ACCTCTAATG GGTCTTCAGC	600
AGGTATTACC GCTGTTAAGG AGAAAACCGC TGATATTGGT ATGGTTTCTA GGGAAATTAAC	660
TCCTGAAGAA GGTAAGAGTC TCACCCATGA TGCTATTGCT TTAGACGGTA TTGCTGTTGT	720
GGTCAATAAT GACAATAAGG CAAGCCAAGT CAGTATGGCT GAACTTGCAG ACGTTTTTAG	780
TGGCAAATTA ACCACCTGGG ACAAGATTAA A	811

## (2) INFORMATION FOR SEQ ID NO:206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Cys	Gly	Asn	Gln	Ser	Ala	Ala	Ser	Lys	Gln	Ser	Ala	Ser	Gly	Thr	Ile	1	5	10	15
Glu	Val	Ile	Ser	Arg	Glu	Asn	Gly	Ser	Gly	Thr	Arg	Gly	Ala	Phe	Thr	20	25	30	
Glu	Ile	Thr	Gly	Ile	Leu	Lys	Lys	Asp	Gly	Asp	Lys	Lys	Ile	Asp	Asn	35	40	45	
Thr	Ala	Lys	Thr	Ala	Val	Ile	Gln	Asn	Ser	Thr	Glu	Gly	Val	Leu	Ser	50	55	60	
Ala	Val	Gln	Gly	Asn	Ala	Asn	Ala	Ile	Gly	Tyr	Ile	Ser	Leu	Gly	Ser	65	70	75	80
Leu	Thr	Lys	Ser	Val	Lys	Ala	Leu	Glu	Ile	Asp	Gly	Val	Lys	Ala	Ser	85	90	95	
Arg	Asp	Thr	Val	Leu	Asp	Gly	Glu	Tyr	Pro	Leu	Gln	Arg	Pro	Phe	Asn	100	105	110	
Ile	Val	Trp	Ser	Ser	Asn	Leu	Ser	Lys	Leu	Gly	Gln	Asp	Phe	Ile	Ser	115	120	125	
Phe	Ile	His	Ser	Lys	Gln	Gly	Gln	Gln	Val	Val	Thr	Asp	Asn	Lys	Phe	130	135	140	
Ile	Glu	Ala	Lys	Thr	Glu	Thr	Thr	Glu	Tyr	Thr	Ser	Gln	His	Leu	Ser	145	150	155	160
Gly	Lys	Leu	Ser	Val	Val	Gly	Ser	Thr	Ser	Val	Ser	Ser	Leu	Met	Glu	165	170	175	
Lys	Leu	Ala	Glu	Ala	Tyr	Lys	Lys	Glu	Asn	Pro	Glu	Val	Thr	Ile	Asp	180	185	190	
Ile	Thr	Ser	Asn	Gly	Ser	Ser	Ala	Gly	Ile	Thr	Ala	Val	Lys	Glu	Lys	195	200	205	
Thr	Ala	Asp	Ile	Gly	Met	Val	Ser	Arg	Glu	Leu	Thr	Pro	Glu	Glu	Gly	210	215	220	
Lys	Ser	Leu	Thr	His	Asp	Ala	Ile	Ala	Leu	Asp	Gly	Ile	Ala	Val	Val	225	230	235	240
Val	Asn	Asn	Asp	Asn	Lys	Ala	Ser	Gln	Val	Ser	Met	Ala	Glu	Leu	Ala	245	250	255	
Asp	Val	Phe	Ser	Gly	Lys	Leu	Thr	Thr	Trp	Asp	Lys	Ile	Lys	260	265	270			

(2) INFORMATION FOR SEQ ID NO: 207:

09765072.012201

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

TTGTCAACAA CAACATGCTA CTTCTGAGGG GACGAATCAA AGGCAAAGCA GTTCAGCGAA 60  
 AGTTCCATGG AAAGCTTCAT ACACCAACCT AAACAACCAG GTAAGTACAG AAGAGGTCAA 120  
 ATCTCTCTTA TCAGCTCACT TGGATCCAAA TAGTGTTGAT GCATTTTTTA ATCTCGTTAA 180  
 TGA CTATAAT ACCATTGTCG GCTCAACTGG CTTATCAGGA GATTTCACTT CCTTTACTCA 240  
 CACCGAATAC GATGTTGAGA AAATCAGTCA TCTCTGGAAT CAAAAGAAGG GCGATTTTGT 300  
 TGGGACCAAC TGCCGTATCA ATAGTTATTG TCTTTTGAAA AATTCAGTCA CCATTCCAAA 360  
 GCTTGAAAAG AATGACCAGT TGCTTTTCCT AGATAATGAT GCGATTGATA AAGGAAAGGT 420  
 CTTTGATTCA CAAGATAAGG AAGAGTTTGA TATTCTATTT TCGAGAGTTC CAACTGAGTC 480  
 AACTACAGAT GTCAAGGTC ACGCTGAAAA GATGGAAGCA TTCTTCTCAC AATTTCAATT 540  
 CAATGAAAAA GCTCGAATGC TGTCTGTAGT CTTGCACGAC AATTTGGATG GCGAGTATCT 600  
 GTTTGTAGGC CACGTTGGGG TCTTAGTACC TGCTGATGAC GGTTTCTTAT TTGTAGAGAA 660  
 ATTGACTTTC GAAGAGCCCT ACCAAGCGAT TAAATTTGCT AGTAAGGAAG ATTGCTACAA 720  
 GTATTTGGGC ACCAAGTATG CGGATTATAC AGGCGAGGGA CTGGCTAAGC CTTTTATCAT 780  
 GGATAATGAT AAGTGGGTTA AACTT 805

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Cys Gln Gln Gln His Ala Thr Ser Glu Gly Thr Asn Gln Arg Gln Ser  
 1 5 10 15  
 Ser Ser Ala Lys Val Pro Trp Lys Ala Ser Tyr Thr Asn Leu Asn Asn  
 20 25 30  
 Gln Val Ser Thr Glu Glu Val Lys Ser Leu Leu Ser Ala His Leu Asp  
 35 40 45  
 Pro Asn Ser Val Asp Ala Phe Phe Asn Leu Val Asn Asp Tyr Asn Thr  
 50 55 60

09765272.012201

Ile Val Gly Ser Thr Gly Leu Ser Gly Asp Phe Thr Ser Phe Thr His  
65 70 75 80

Thr Glu Tyr Asp Val Glu Lys Ile Ser His Leu Trp Asn Gln Lys Lys  
85 90 95

Gly Asp Phe Val Gly Thr Asn Cys Arg Ile Asn Ser Tyr Cys Leu Leu  
100 105 110

Lys Asn Ser Val Thr Ile Pro Lys Leu Glu Lys Asn Asp Gln Leu Leu  
115 120 125

Phe Leu Asp Asn Asp Ala Ile Asp Lys Gly Lys Val Phe Asp Ser Gln  
130 135 140

Asp Lys Glu Glu Phe Asp Ile Leu Phe Ser Arg Val Pro Thr Glu Ser  
145 150 155 160

Thr Thr Asp Val Lys Val His Ala Glu Lys Met Glu Ala Phe Phe Ser  
165 170 175

Gln Phe Gln Phe Asn Glu Lys Ala Arg Met Leu Ser Val Val Leu His  
180 185 190

Asp Asn Leu Asp Gly Glu Tyr Leu Phe Val Gly His Val Gly Val Leu  
195 200 205

Val Pro Ala Asp Asp Gly Phe Leu Phe Val Glu Lys Leu Thr Phe Glu  
210 215 220

Glu Pro Tyr Gln Ala Ile Lys Phe Ala Ser Lys Glu Asp Cys Tyr Lys  
225 230 235 240

Tyr Leu Gly Thr Lys Tyr Ala Asp Tyr Thr Gly Glu Gly Leu Ala Lys  
245 250 255

Pro Phe Ile Met Asp Asn Asp Lys Trp Val Lys Leu  
260 265

## (2) INFORMATION FOR SEQ ID NO: 209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TTGTTTCAGGC AAGTCCGTGA CTAGTGAACA CCAAACGAAA GATGAAATGA AGACGGAGCA	60
GACAGCTAGT AAAACAAGCG CAGCTAAAGG GAAAGAGGTG GCTGATTTTG AATTGATGGG	120
AGTAGATGGC AAGACCTACC GTTTATCTGA TTACAAGGGC AAGAAAGTCT ATCTCAAATT	180
CTGGGCTTCT TGGTGTTCCTA TCTGTCTGGC TAGTCTTCCA GATACGGATG AGATTGCTAA	240
AGAAGCTGGT GATGACTATG TGGTCTTGAC AGTAGTGTCA CCAGGACATA AGGGAGAGCA	300
ATCTGAAGCG GACTTTAAGA ATTGGTATAA GGGATTGGAT TATAAAAATC TCCAGTCTCT	360

09765272-012201

AGTTGACCCA TCAGGCAAAC TTTTGAAAC TTATGGTGTC CGTTCTTACC CAACCCAAGC 420  
 CTTTATAGAC AAAGAAGGCA AGCTGGTCAA AACACATCCA GGATTCATGG AAAAAGATGC 480  
 AATTTTGCAA ACTTTGAAGG AATTAGCC 508

## (2) INFORMATION FOR SEQ ID NO:210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Cys Ser Gly Lys Ser Val Thr Ser Glu His Gln Thr Lys Asp Glu Met  
 1 5 10 15  
 Lys Thr Glu Gln Thr Ala Ser Lys Thr Ser Ala Ala Lys Gly Lys Glu  
 20 25 30  
 Val Ala Asp Phe Glu Leu Met Gly Val Asp Gly Lys Thr Tyr Arg Leu  
 35 40 45  
 Ser Asp Tyr Lys Gly Lys Lys Val Tyr Leu Lys Phe Trp Ala Ser Trp  
 50 55 60  
 Cys Ser Ile Cys Leu Ala Ser Leu Pro Asp Thr Asp Glu Ile Ala Lys  
 65 70 75 80  
 Glu Ala Gly Asp Asp Tyr Val Val Leu Thr Val Val Ser Pro Gly His  
 85 90 95  
 Lys Gly Glu Gln Ser Glu Ala Asp Phe Lys Asn Trp Tyr Lys Gly Leu  
 100 105 110  
 Asp Tyr Lys Asn Leu Pro Val Leu Val Asp Pro Ser Gly Lys Leu Leu  
 115 120 125  
 Glu Thr Tyr Gly Val Arg Ser Tyr Pro Thr Gln Ala Phe Ile Asp Lys  
 130 135 140  
 Glu Gly Lys Leu Val Lys Thr His Pro Gly Phe Met Glu Lys Asp Ala  
 145 150 155 160  
 Ile Leu Gln Thr Leu Lys Glu Leu Ala  
 165

## (2) INFORMATION FOR SEQ ID NO: 211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

09765072.012201



CTCGCAAATT GAAAAGGCGG CAGTTAGCCA AGGAGGAAAA GCAGTGAAAA AACAGAAAT 60  
 TAGTAAAGAC GCAGACTTGC ACGAAATTTA TCTAGCTGGA GGTGTTTCT GGGGAGTGGA 120  
 GGAATATTTT TCACGTGTTT CCGGGGTGAC GGATGCCGTT TCAGGCTATG CAAATGGTAG 180  
 AGGAGAAACA ACCAAGTACG AATTGATTAA CCAAACAGGT CATGCAGAAA CCGTCCATGT 240  
 CACCTATGAT GCCAAGCAAA TTTCTCTCAA GGAAATCCTG CTTCACTATT TCCGCATTAT 300  
 CAATCCAACC AGCAAAAATA AACAAGGAAA TGATGTGGGG ACCCAGTACC GTACTGGTGT 360  
 TTATTACACA GATGACAAGG ATTTGGAAGT GATTAACCAA GTCTTTGATG AGGTGGCTAA 420  
 GAAATACGAT CAACCTCTAG CAGTTGAAAA GGAAACTTG AAGAATTTTG TGGTGGCTGA 480  
 GGATTACCAT CAAGACTATC TCAAGAAAAA TCCAAATGGC TACTGCCATA TCAATGTTAA 540  
 TCAGGCGGCC TATCCTGTCA TTGATGCCAG CAAATATCCA AAACCAAGTG ATGAGGAATT 600  
 GAAAAAGACC CTGTCACCTG AGGAGTATGC AGTTACCCAG GAAAATCAAA CAGAACGAGC 660  
 TTTCTCAAAC CGTTACTGGG ATAAATTTGA ATCCGGTATC TATGTGGATA TAGCAACTGG 720  
 GGAACCTCTC TTTTCATCAA AAGACAAATT TGAGTCTGGT TGTGGCTGGC CTAGTTTAC 780  
 CCAACCCATC AGTCCAGATG TTGTCACCTA CAAGGAAGAT AAGTCCTACA ATATGACGCG 840  
 TATGGAAGTG CGGAGCCGAG TAGGAGATTC TCACCTTGGG CATGTCTTTA CGGATGGTCC 900  
 ACAGGACAAG GGCGGCTTAC GTTACTGTAT CAATAGCCTC TCTATCCGCT TTATTCCCAA 960  
 AGACCAAATG GAAGAAAAAG GTACGCTTAT TTAC 994

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ser	Gln	Ile	Glu	Lys	Ala	Ala	Val	Ser	Gln	Gly	Gly	Lys	Ala	Val	Lys
1				5				10				15			
Lys	Thr	Glu	Ile	Ser	Lys	Asp	Ala	Asp	Leu	His	Glu	Ile	Tyr	Leu	Ala
		20					25					30			
Gly	Gly	Cys	Phe	Trp	Gly	Val	Glu	Glu	Tyr	Phe	Ser	Arg	Val	Pro	Gly
		35				40					45				
Val	Thr	Asp	Ala	Val	Ser	Gly	Tyr	Ala	Asn	Gly	Arg	Gly	Glu	Thr	Thr
	50					55				60					
Lys	Tyr	Glu	Leu	Ile	Asn	Gln	Thr	Gly	His	Ala	Glu	Thr	Val	His	Val
65					70				75					80	

09765272 012201

315

Thr Tyr Asp Ala Lys Gln Ile Ser Leu Lys Glu Ile Leu Leu His Tyr  
85 90 95

Phe Arg Ile Ile Asn Pro Thr Ser Lys Asn Lys Gln Gly Asn Asp Val  
100 105 110

Gly Thr Gln Tyr Arg Thr Gly Val Tyr Tyr Thr Asp Asp Lys Asp Leu  
115 120 125

Glu Val Ile Asn Gln Val Phe Asp Glu Val Ala Lys Lys Tyr Asp Gln  
130 135 140

Pro Leu Ala Val Glu Lys Glu Asn Leu Lys Asn Phe Val Val Ala Glu  
145 150 155 160

Asp Tyr His Gln Asp Tyr Leu Lys Lys Asn Pro Asn Gly Tyr Cys His  
165 170 175

Ile Asn Val Asn Gln Ala Ala Tyr Pro Val Ile Asp Ala Ser Lys Tyr  
180 185 190

Pro Lys Pro Ser Asp Glu Glu Leu Lys Lys Thr Leu Ser Pro Glu Glu  
195 200 205

Tyr Ala Val Thr Gln Glu Asn Gln Thr Glu Arg Ala Phe Ser Asn Arg  
210 215 220

Tyr Trp Asp Lys Phe Glu Ser Gly Ile Tyr Val Asp Ile Ala Thr Gly  
225 230 235 240

Glu Pro Leu Phe Ser Ser Lys Asp Lys Phe Glu Ser Gly Cys Gly Trp  
245 250 255

Pro Ser Phe Thr Gln Pro Ile Ser Pro Asp Val Val Thr Tyr Lys Glu  
260 265 270

Asp Lys Ser Tyr Asn Met Thr Arg Met Glu Val Arg Ser Arg Val Gly  
275 280 285

Asp Ser His Leu Gly His Val Phe Thr Asp Gly Pro Gln Asp Lys Gly  
290 295 300

Gly Leu Arg Tyr Cys Ile Asn Ser Leu Ser Ile Arg Phe Ile Pro Lys  
305 310 315 320

Asp Gln Met Glu Glu Lys Gly Thr Leu Ile Tyr  
325 330

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 625 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TTGTCAGTCA GGTTC TAATG GTTCTCAGTC TGCTGTGGAT GCTATCAAAC AAAAAGGGAA 60

ATTAGTTGTG GCAACCAGTC CTGACTATGC ACCCTTTGAA TTTCAATCAT TGGTTGATGG 120

09765272.012201

AAAGAACCAG GTAGTCGGTG CAGACATCGA CATGGCTCAG GCTATCGCTG ATGAACTTGG 180  
 GGTAAAGTTG GAAATCTCAA GCATGAGTTT TGACAATGTT TTGACCAGTC TTCAAAGTGG 240  
 TAAGGCTGAC CTAGCAGTTG CAGGAATTAG TGCTACTGAC GAGAGAAAAG AAGTCTTTGA 300  
 TTTTTCATC CCATACTATG AAAACAAGAT TAGTTTCTTG GTTCGTAAGG CTGATGTGGA 360  
 AAAATACAAG GATTTAAC TA GCCTAGAAAG TGCTAATATT GCAGCCCAA AAGGGACTGT 420  
 TCCAGAATCA ATGGTCAAGG AACAATTGCC AAAAGTTCAA TTAAGTTCCC TAACTAATAT 480  
 GGGTGAAGCA GTCAATGAAT TGCAGGCTGG AAAAATAGAT GCTGTTTCATA TGGATGAGCC 540  
 TGTTCACCTT AGTTATGCTG CTAAAAACGC TGGCTTAGCT GTCGCAACTG TCAGCTTGAA 600  
 GATGAAGGAC GCGCAGGCCA ATGCC 625

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Cys Gln Ser Gly Ser Asn Gly Ser Gln Ser Ala Val Asp Ala Ile Lys  
 1 5 10 15  
 Gln Lys Gly Lys Leu Val Val Ala Thr Ser Pro Asp Tyr Ala Pro Phe  
 20 25 30  
 Glu Phe Gln Ser Leu Val Asp Gly Lys Asn Gln Val Val Gly Ala Asp  
 35 40 45  
 Ile Asp Met Ala Gln Ala Ile Ala Asp Glu Leu Gly Val Lys Leu Glu  
 50 55 60  
 Ile Ser Ser Met Ser Phe Asp Asn Val Leu Thr Ser Leu Gln Thr Gly  
 65 70 75 80  
 Lys Ala Asp Leu Ala Val Ala Gly Ile Ser Ala Thr Asp Glu Arg Lys  
 85 90 95  
 Glu Val Phe Asp Phe Ser Ile Pro Tyr Tyr Glu Asn Lys Ile Ser Phe  
 100 105 110  
 Leu Val Arg Lys Ala Asp Val Glu Lys Tyr Lys Asp Leu Thr Ser Leu  
 115 120 125  
 Glu Ser Ala Asn Ile Ala Ala Gln Lys Gly Thr Val Pro Glu Ser Met  
 130 135 140  
 Val Lys Glu Gln Leu Pro Lys Val Gln Leu Thr Ser Leu Thr Asn Met  
 145 150 155 160  
 Gly Glu Ala Val Asn Glu Leu Gln Ala Gly Lys Ile Asp Ala Val His

09765272.012201

165

170

175

Met Asp Glu Pro Val Ala Leu Ser Tyr Ala Ala Lys Asn Ala Gly Leu  
 180 185 190

Ala Val Ala Thr Val Ser Leu Lys Met Lys Asp Gly Asp Ala Asn Ala  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO: 215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

GGAAACTTCA CAGGATTTTA AAGAGAAGAA AACAGCAGTC ATTAAGGAAA AAGAAGTTGT	60
TAGTAAAAAT CCTGTGATAG ACAATAACAC TAGCAATGAA GAAGCAAAAA TCAAAGAAGA	120
AAATTCCAAT AAATCCCAAG GAGATTATAC GGACTCATTT GTGAATAAAA ACACAGAAAA	180
TCCCCAAAAA GAAGATAAAG TTGTCTATAT TGCTGAATTT AAAGATAAAG AATCTGGAGA	240
AAAAGCAATC AAGGAACTAT CCAGTCTTAA GAATACAAAA GTTTTATATA CTTATGATAG	300
AATTTTAAAC GGTAGTGCCA TAGAAACAAC TCCAGATAAC TTGGACAAAA TTAAACAAAT	360
AGAAGGTATT TCATCGGTTG AAAGGGCACA AAAAGTCCAA CCCATGATGA ATCATGCCAG	420
AAAGGAAATT GGAGTTGAGG AAGCTATTGA TTACCTAAAG TCTATCAATG CTCCGTTTGG	480
GAAAAATTTT GATGGTAGAG GTATGGTCAT TTCAAATATC GATACTGGAA CAGATTATAG	540
ACATAAGGCT ATGAGAATCG ATGATGATGC CAAAGCCTCA ATGAGATTTA AAAAAGAAGA	600
CTTAAAAGGC ACTGATAAAA ATTATTGGTT GAGTGATAAA ATCCCTCATG CGTTCAATTA	660
TTATAATGGT GGCAAAATCA CTGTAGAAAA ATATGATGAT GGAAGGGATT ATTTTGACCC	720
ACATGGGATG CATATTGCAG GGATTCTTGC TGGAAATGAT ACTGAACAAG ACATCAAAAA	780
CTTTAACGGC ATAGATGGAA TTGCACCTAA TGCACAAATT TTCTCTTACA AAATGTATTC	840
TGACGCAGGA TCTGGGTTTG CGGGTGATGA AACAATGTTT CATGCTATTG AAGATTCTAT	900
CAAACACAAC GTTGATGTTG TTTCGGTATC ATCTGGTTTT ACAGGAACAG GTCTTGTAGG	960
TGAGAAATAT TGGCAAGCTA TTCGGGCATT AAGAAAAGCA GGCATTCCAA TGGTTGTCGC	1020
TACGGGTAAC TATGCGACTT CTGCTTCAAG TTCTTCATGG GATTTAGTAG CAAATAATCA	1080
TCTGAAAATG ACCGACACTG GAAATGTAAC ACGAACTGCA GCACATGAAG ATGCGATAGC	1140
GGTCGCTTCT GCTAAAAATC AAACAGTTGA GTTTGATAAA GTTAACATAG GTGGAGAAAG	1200
TTTTAAATAC AGAAATATAG GGGCCTTTTT CGATAAGAGT AAAATCACAA CAAATGAAGA	1260
TGGAACAAAA GCTCCTAGTA AATTAAATTT TGTATATATA GGCAAGGGGC AAGACCAAGA	1320

00765272.012201

TTTGATAGGT TTGGATCTTA GGGGCAAAAT TGCAGTAATG GATAGAATTT ATACAAAGGA 1380  
 TTTAAAAAAT GCTTTTAAAA AAGCTATGGA TAAGGGTGCA CGCGCCATTA TGGTTGTAAA 1440  
 TACTGTAAAT TACTACAATA GAGATAATTG GACAGAGCTT CCAGCTATGG GATATGAAGC 1500  
 GGATGAAGGT ACTAAAAGTC AAGTGTTTTT AATTTTCAGGA GATGATGGTG TAAAGCTATG 1560  
 GAACATGATT AATCCTGATA AAAAACTGA AGTCAAAAGA AATAATAAAG AAGATTTTAA 1620  
 AGATAAATTG GAGCAATACT ATCCAATTGA TATGGAAAGT TTTAATTCCA ACAAACCGAA 1680  
 TGTAGGTGAC GAAAAAGAGA TTGACTTTAA GTTTGCACCT GACACAGACA AAGAACTCTA 1740  
 TAAAGAAGAT ATCATCGTTC CAGCAGGATC TACATCTTGG GGGCCAAGAA TAGATTTACT 1800  
 TTTAAAACCC GATGTTTTAG CACCTGGTAA AAATATTAAA TCCACGCTTA ATGTTATTAA 1860  
 TGGCAAATCA ACTTATGGCT ATATGTCAGG AACTAGTATG GCGACTCCAA TCGTGGCAGC 1920  
 TTCTACTGTT TTGATTAGAC CGAAATTAAA GGAAATGCTT GAAAGACCTG TATTGAAAAA 1980  
 TCTTAAGGGA GATGACAAAA TAGATCTTAC AAGTCTTACA AAAATTGCCC TACAAAATAC 2040  
 TGCGCGACCT ATGATGGATG CAACTTCTTG GAAAGAAAAA AGTCAATACT TTGCATCACC 2100  
 TAGACAACAG GGAGCAGGCC TAATTAATGT GGCCAATGCT TTGAGAAATG AAGTTGTAGC 2160  
 AACTTTCAAA AACACTGATT CTAAAGGTTT GGTAAACTCA TATGGTTCCA TTTCTCTTAA 2220  
 AGAAATAAAA GGTGATAAAA AATACTTTAC AATCAAGCTT CACAATACAT CAAACAGACC 2280  
 TTTGACTTTT AAAGTTTCAG CATCAGCGAT AACTACAGAT TCTCTAACTG ACAGATTAAA 2340  
 ACTTGATGAA ACATATAAAG ATGAAAAATC TCCAGATGGT AAGCAAATTG TTCCAGAAAT 2400  
 TCACCCAGAA AAAGTCAAAG GAGCAAATAT CACATTTGAG CATGATACTT TCACTATAGG 2460  
 CGCAAATTCT AGCTTTGATT TGAATGCGGT TATAAATGTT GGAGAGGCCA AAAACAAAAA 2520  
 TAAATTTGTA GAATCATTTA TTCATTTTGA GTCAGTGGAA GCGATGGAAG CTCTAAACTC 2580  
 CAGCGGGAAG AAAATAAACT TCCAACCTTC TTTGTCGATG CCTCTAATGG GATTTGCTGG 2640  
 GAATTGGAAC CACGAACCAA TCCTTGATAA ATGGGCTTGG GAAGAAGGGT CAAGATCAAA 2700  
 AACACTGGGA GGTTATGATG ATGATGGTAA ACCGAAAATT CCAGGAACCT TAAATAAGGG 2760  
 AATTGGTGGA GAACATGGTA TAGATAAATT TAATCCAGCA GGAGTTATAC AAAATAGAAA 2820  
 AGATAAAAAT ACAACATCCC TGGATCAAAA TCCAGAATTA TTTGCTTTCA ATAACGAAGG 2880  
 GATCAACGCT CCATCATCAA GTGGTTCTAA GATTGCTAAC ATTTATCCTT TAGATTCAAA 2940  
 TGGAAATCCT CAAGATGCTC AACTTGAAAG AGGATTAACA CCTTCTCCAC TTGTATTAAG 3000  
 AAGTGCAGAA GAAGGATTGA TT 3022

## (2) INFORMATION FOR SEQ ID NO:216:

## (i). SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1007 amino acids

09765272.012201

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Glu	Thr	Ser	Gln	Asp	Phe	Lys	Glu	Lys	Lys	Thr	Ala	Val	Ile	Lys	Glu	1	5	10	15
Lys	Glu	Val	Val	Ser	Lys	Asn	Pro	Val	Ile	Asp	Asn	Asn	Thr	Ser	Asn	20	25	30	
Glu	Glu	Ala	Lys	Ile	Lys	Glu	Glu	Asn	Ser	Asn	Lys	Ser	Gln	Gly	Asp	35	40	45	
Tyr	Thr	Asp	Ser	Phe	Val	Asn	Lys	Asn	Thr	Glu	Asn	Pro	Lys	Lys	Glu	50	55	60	
Asp	Lys	Val	Val	Tyr	Ile	Ala	Glu	Phe	Lys	Asp	Lys	Glu	Ser	Gly	Glu	65	70	75	80
Lys	Ala	Ile	Lys	Glu	Leu	Ser	Ser	Leu	Lys	Asn	Thr	Lys	Val	Leu	Tyr	85	90	95	
Thr	Tyr	Asp	Arg	Ile	Phe	Asn	Gly	Ser	Ala	Ile	Glu	Thr	Thr	Pro	Asp	100	105	110	
Asn	Leu	Asp	Lys	Ile	Lys	Gln	Ile	Glu	Gly	Ile	Ser	Ser	Val	Glu	Arg	115	120	125	
Ala	Gln	Lys	Val	Gln	Pro	Met	Met	Asn	His	Ala	Arg	Lys	Glu	Ile	Gly	130	135	140	
Val	Glu	Glu	Ala	Ile	Asp	Tyr	Leu	Lys	Ser	Ile	Asn	Ala	Pro	Phe	Gly	145	150	155	160
Lys	Asn	Phe	Asp	Gly	Arg	Gly	Met	Val	Ile	Ser	Asn	Ile	Asp	Thr	Gly	165	170	175	
Thr	Asp	Tyr	Arg	His	Lys	Ala	Met	Arg	Ile	Asp	Asp	Asp	Ala	Lys	Ala	180	185	190	
Ser	Met	Arg	Phe	Lys	Lys	Glu	Asp	Leu	Lys	Gly	Thr	Asp	Lys	Asn	Tyr	195	200	205	
Trp	Leu	Ser	Asp	Lys	Ile	Pro	His	Ala	Phe	Asn	Tyr	Tyr	Asn	Gly	Gly	210	215	220	
Lys	Ile	Thr	Val	Glu	Lys	Tyr	Asp	Asp	Gly	Arg	Asp	Tyr	Phe	Asp	Pro	225	230	235	240
His	Gly	Met	His	Ile	Ala	Gly	Ile	Leu	Ala	Gly	Asn	Asp	Thr	Glu	Gln	245	250	255	
Asp	Ile	Lys	Asn	Phe	Asn	Gly	Ile	Asp	Gly	Ile	Ala	Pro	Asn	Ala	Gln	260	265	270	
Ile	Phe	Ser	Tyr	Lys	Met	Tyr	Ser	Asp	Ala	Gly	Ser	Gly	Phe	Ala	Gly	275	280	285	

097655272 0122001

Asp Glu Thr Met Phe His Ala Ile Glu Asp Ser Ile Lys His Asn Val  
 290 295 300  
 Asp Val Val Ser Val Ser Ser Gly Phe Thr Gly Thr Gly Leu Val Gly  
 305 310 315 320  
 Glu Lys Tyr Trp Gln Ala Ile Arg Ala Leu Arg Lys Ala Gly Ile Pro  
 325 330 335  
 Met Val Val Ala Thr Gly Asn Tyr Ala Thr Ser Ala Ser Ser Ser  
 340 345 350  
 Trp Asp Leu Val Ala Asn Asn His Leu Lys Met Thr Asp Thr Gly Asn  
 355 360 365  
 Val Thr Arg Thr Ala Ala His Glu Asp Ala Ile Ala Val Ala Ser Ala  
 370 375 380  
 Lys Asn Gln Thr Val Glu Phe Asp Lys Val Asn Ile Gly Gly Glu Ser  
 385 390 395 400  
 Phe Lys Tyr Arg Asn Ile Gly Ala Phe Phe Asp Lys Ser Lys Ile Thr  
 405 410 415  
 Thr Asn Glu Asp Gly Thr Lys Ala Pro Ser Lys Leu Lys Phe Val Tyr  
 420 425 430  
 Ile Gly Lys Gly Gln Asp Gln Asp Leu Ile Gly Leu Asp Leu Arg Gly  
 435 440 445  
 Lys Ile Ala Val Met Asp Arg Ile Tyr Thr Lys Asp Leu Lys Asn Ala  
 450 455 460  
 Phe Lys Lys Ala Met Asp Lys Gly Ala Arg Ala Ile Met Val Val Asn  
 465 470 475 480  
 Thr Val Asn Tyr Tyr Asn Arg Asp Asn Trp Thr Glu Leu Pro Ala Met  
 485 490 495  
 Gly Tyr Glu Ala Asp Glu Gly Thr Lys Ser Gln Val Phe Ser Ile Ser  
 500 505 510  
 Gly Asp Asp Gly Val Lys Leu Trp Asn Met Ile Asn Pro Asp Lys Lys  
 515 520 525  
 Thr Glu Val Lys Arg Asn Asn Lys Glu Asp Phe Lys Asp Lys Leu Glu  
 530 535 540  
 Gln Tyr Tyr Pro Ile Asp Met Glu Ser Phe Asn Ser Asn Lys Pro Asn  
 545 550 555 560  
 Val Gly Asp Glu Lys Glu Ile Asp Phe Lys Phe Ala Pro Asp Thr Asp  
 565 570 575  
 Lys Glu Leu Tyr Lys Glu Asp Ile Ile Val Pro Ala Gly Ser Thr Ser  
 580 585 590  
 Trp Gly Pro Arg Ile Asp Leu Leu Leu Lys Pro Asp Val Ser Ala Pro  
 595 600 605  
 Gly Lys Asn Ile Lys Ser Thr Leu Asn Val Ile Asn Gly Lys Ser Thr  
 610 615 620

00765072.012201

Tyr	Gly	Tyr	Met	Ser	Gly	Thr	Ser	Met	Ala	Thr	Pro	Ile	Val	Ala	Ala	
625					630					635					640	
Ser	Thr	Val	Leu	Ile	Arg	Pro	Lys	Leu	Lys	Glu	Met	Leu	Glu	Arg	Pro	
				645					650					655		
Val	Leu	Lys	Asn	Leu	Lys	Gly	Asp	Asp	Lys	Ile	Asp	Leu	Thr	Ser	Leu	
			660					665					670			
Thr	Lys	Ile	Ala	Leu	Gln	Asn	Thr	Ala	Arg	Pro	Met	Met	Asp	Ala	Thr	
		675					680					685				
Ser	Trp	Lys	Glu	Lys	Ser	Gln	Tyr	Phe	Ala	Ser	Pro	Arg	Gln	Gln	Gly	
	690					695					700					
Ala	Gly	Leu	Ile	Asn	Val	Ala	Asn	Ala	Leu	Arg	Asn	Glu	Val	Val	Ala	
705				710						715					720	
Thr	Phe	Lys	Asn	Thr	Asp	Ser	Lys	Gly	Leu	Val	Asn	Ser	Tyr	Gly	Ser	
				725					730					735		
Ile	Ser	Leu	Lys	Glu	Ile	Lys	Gly	Asp	Lys	Lys	Tyr	Phe	Thr	Ile	Lys	
			740					745					750			
Leu	His	Asn	Thr	Ser	Asn	Arg	Pro	Leu	Thr	Phe	Lys	Val	Ser	Ala	Ser	
		755					760					765				
Ala	Ile	Thr	Thr	Asp	Ser	Leu	Thr	Asp	Arg	Leu	Lys	Leu	Asp	Glu	Thr	
	770					775					780					
Tyr	Lys	Asp	Glu	Lys	Ser	Pro	Asp	Gly	Lys	Gln	Ile	Val	Pro	Glu	Ile	
785					790					795					800	
His	Pro	Glu	Lys	Val	Lys	Gly	Ala	Asn	Ile	Thr	Phe	Glu	His	Asp	Thr	
				805					810					815		
Phe	Thr	Ile	Gly	Ala	Asn	Ser	Ser	Phe	Asp	Leu	Asn	Ala	Val	Ile	Asn	
			820					825					830			
Val	Gly	Glu	Ala	Lys	Asn	Lys	Asn	Lys	Phe	Val	Glu	Ser	Phe	Ile	His	
		835					840					845				
Phe	Glu	Ser	Val	Glu	Ala	Met	Glu	Ala	Leu	Asn	Ser	Ser	Gly	Lys	Lys	
	850					855					860					
Ile	Asn	Phe	Gln	Pro	Ser	Leu	Ser	Met	Pro	Leu	Met	Gly	Phe	Ala	Gly	
865					870					875					880	
Asn	Trp	Asn	His	Glu	Pro	Ile	Leu	Asp	Lys	Trp	Ala	Trp	Glu	Glu	Gly	
				885					890					895		
Ser	Arg	Ser	Lys	Thr	Leu	Gly	Gly	Tyr	Asp	Asp	Asp	Gly	Lys	Pro	Lys	
			900					905					910			
Ile	Pro	Gly	Thr	Leu	Asn	Lys	Gly	Ile	Gly	Gly	Glu	His	Gly	Ile	Asp	
		915					920					925				
Lys	Phe	Asn	Pro	Ala	Gly	Val	Ile	Gln	Asn	Arg	Lys	Asp	Lys	Asn	Thr	
	930					935					940					
Thr	Ser	Leu	Asp	Gln	Asn	Pro	Glu	Leu	Phe	Ala	Phe	Asn	Asn	Glu	Gly	
945					950					955					960	

09765272 012201



Ile Asn Ala Pro Ser Ser Ser Gly Ser Lys Ile Ala Asn Ile Tyr Pro  
 965 970 975

Leu Asp Ser Asn Gly Asn Pro Gln Asp Ala Gln Leu Glu Arg Gly Leu  
 980 985 990

Thr Pro Ser Pro Leu Val Leu Arg Ser Ala Glu Glu Gly Leu Ile  
 995 1000 1005

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

TGTGGTCGAA GTTGAGACTC CTCAATCAAT AACAAATCAG GAGCAAGCTA GGACAGAAAA	60
CCAAGTAGTA GAGACAGAGG AAGCTCCAAA AGAAGAAGCA CCTAAAACAG AAGAAAGTCC	120
AAAGGAAGAA CCAAATCGG AGGTAAACC TACTGACGAC ACCCTTCCTA AAGTAGAAGA	180
GGGGAAGAA GATTGAGCAG AACCAGCTCC AGTTGAAGAA GTAGGTGGAG AAGTTGAGTC	240
AAAACCAGAG GAAAAAGTAG CAGTTAAGCC AGAAAGTCAA CCATCAGACA AACCAGCTGA	300
GGAATCAAAA GTTGAACAAG CAGGTGAACC AGTCGCGCCA AGAGAAGACG AAAAGGCACC	360
AGTCGAGCCA GAAAGCAAC CAGAAGCTCC TGAAGAAGAG AAGGCTGTAG AGGAAACACC	420
GAAACAAGAA GAGTCAACTC CAGATACCAA GGCTGAAGAA ACTGTAGAAC CAAAAGAGGA	480
GACTGTTAAT CAATCTATTG AACAACCAA AGTTGAAACG CCTGCTGTAG AAAACAAAC	540
AGAACCAACA GAGGAACCAA AAGTTGAACA AGCAGGTGAA CCAGTCGCGC CAAGAGAAGA	600
CGAACAGGCA CCAACGGCAC CAGTTGAGCC AGAAAAGCAA CCAGAAGTTC CTGAAGAAGA	660
GAAGGCTGTA GAGGAAACAC CGAAACCAGA AGATAAAATA AAGGGTATTG GTACTAAAGA	720
ACCAGTTGAT AAAAGTGAGT TAAATAATCA AATTGATAAA GCTAGTTCAG TTTCTCCTAC	780
TGATTATTCT ACAGCAAGTT ACAATGCTCT TGGACCTGTT TTAGAAACTG CAAAAGGTGT	840
CTATGCTTCA GAGCCTGTAA AACAGCCTGA GGTAAATAGC GAGACAAATA AACTTAAAC	900
GGCTATTGAC GCTCTAAACG TTGATAAAAC TGAATTAAAC AATACGATTG CAGATGCAAA	960
AACAAAGGTA AAAGAACATT ACAGTGATAG AAGTTGGCAA AACCTCCAAA CTGAAGTTAC	1020
AAAGGCTGAA AAAGTTGCAG CTAATACAGA TGCTAAACAA AGTGAAGTTA ACGAAGCTGT	1080
TGAAAAATTA ACTGCAACTA TTGAAAAATT GGTGAATTA TCTGAAAAGC CAATATTAAC	1140
ATTGACTAGT ACCGATAAGA AAATATTGGA ACGTGAAGCT GTTGCTAAGT ATACTCTAGA	1200
AAATCAAAAC AAAACAAAAA TCAAATCAAT CACAGCTGAA TTGAAAAAAG GAGAAGAAGT	1260

00765272.012201

TATTAATACT GTAGTCCTTA CAGATGACAA GGTAACAACA GAAACTATAA GCGCTGCATT 1320  
 TAAGAACCTA GAGTACTACA AAGAATACAC CCTATCTACA ACTATGATTT ACGACAGAGG 1380  
 TAACGGTGAA GAAACTGAAA CTCTAGAAAA TCAAAATATT CAATTAGATC TTAAAAAAGT 1440  
 TGAGCTTAAA AATATTAAAC GTACAGATTT AATCAAATAC GAAAATGGAA AAGAAACTAA 1500  
 TGAATCACTG ATAACAACATA TTCCTGATGA TAAGAGCAAT TATTATTTAA AAATAACTTC 1560  
 AAATAATCAG AAAACTACAT TACTAGCTGT TAAAAATATA GAAGAAACTA CGGTAAACGG 1620  
 AACACCTGTA TATAAAGTTA CAGCAATCGC AGACAATTTA GTCTCTAGAA CTGCTGATAA 1680  
 TAAATTTGAA GAAGAA 1696

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Val Val Glu Val Glu Thr Pro Gln Ser Ile Thr Asn Gln Glu Gln Ala  
 1 5 10 15  
 Arg Thr Glu Asn Gln Val Val Glu Thr Glu Glu Ala Pro Lys Glu Glu  
 20 25 30  
 Ala Pro Lys Thr Glu Glu Ser Pro Lys Glu Glu Pro Lys Ser Glu Val  
 35 40 45  
 Lys Pro Thr Asp Asp Thr Leu Pro Lys Val Glu Glu Gly Lys Glu Asp  
 50 55 60  
 Ser Ala Glu Pro Ala Pro Val Glu Glu Val Gly Gly Glu Val Glu Ser  
 65 70 75 80  
 Lys Pro Glu Glu Lys Val Ala Val Lys Pro Glu Ser Gln Pro Ser Asp  
 85 90 95  
 Lys Pro Ala Glu Glu Ser Lys Val Glu Gln Ala Gly Glu Pro Val Ala  
 100 105 110  
 Pro Arg Glu Asp Glu Lys Ala Pro Val Glu Pro Glu Lys Gln Pro Glu  
 115 120 125  
 Ala Pro Glu Glu Glu Lys Ala Val Glu Glu Thr Pro Lys Gln Glu Glu  
 130 135 140  
 Ser Thr Pro Asp Thr Lys Ala Glu Glu Thr Val Glu Pro Lys Glu Glu  
 145 150 155 160  
 Thr Val Asn Gln Ser Ile Glu Gln Pro Lys Val Glu Thr Pro Ala Val  
 165 170 175  
 Glu Lys Gln Thr Glu Pro Thr Glu Glu Pro Lys Val Glu Gln Ala Gly

09765072.012201

	180		185		190
Glu Pro Val	Ala Pro Arg	Glu Asp	Glu Gln Ala	Pro Thr Ala	Pro Val
195		200		205	
Glu Pro Glu	Lys Gln Pro	Glu Val	Pro Glu Glu	Glu Lys Ala	Val Glu
210		215		220	
Glu Thr Pro	Lys Pro	Glu Asp	Lys Ile Lys	Gly Ile Gly	Thr Lys Glu
225		230		235	240
Pro Val Asp	Lys Ser	Glu Leu	Asn Asn	Gln Ile Asp	Lys Ala Ser Ser
	245		250		255
Val Ser Pro	Thr Asp Tyr	Ser Thr	Ala Ser Tyr	Asn Ala Leu	Gly Pro
	260		265		270
Val Leu Glu	Thr Ala Lys	Gly Val	Tyr Ala Ser	Glu Pro Val	Lys Gln
	275		280		285
Pro Glu Val	Asn Ser	Glu Thr	Asn Lys Leu	Lys Thr Ala	Ile Asp Ala
	290		295		300
Leu Asn Val	Asp Lys	Thr Glu	Leu Asn Asn	Thr Ile Ala	Asp Ala Lys
305		310		315	320
Thr Lys Val	Lys Glu	His Tyr	Ser Asp Arg	Ser Trp Gln	Asn Leu Gln
	325		330		335
Thr Glu Val	Thr Lys	Ala Glu	Lys Val Ala	Ala Asn Thr	Asp Ala Lys
	340		345		350
Gln Ser Glu	Val Asn	Glu Ala	Val Glu	Lys Leu Thr	Ala Thr Ile Glu
	355		360		365
Lys Leu Val	Glu Leu	Ser Glu	Lys Pro Ile	Leu Thr Leu	Thr Ser Thr
	370		375		380
Asp Lys Lys	Ile Leu	Glu Arg	Glu Ala Val	Ala Lys Tyr	Thr Leu Glu
385		390		395	400
Asn Gln Asn	Lys Thr	Lys Ile	Lys Ser Ile	Thr Ala Glu	Leu Lys Lys
	405		410		415
Gly Glu Glu	Val Ile	Asn Thr	Val Val	Leu Thr Asp	Asp Lys Val Thr
	420		425		430
Thr Glu Thr	Ile Ser	Ala Ala	Phe Lys	Asn Leu Glu	Tyr Tyr Lys Glu
	435		440		445
Tyr Thr Leu	Ser Thr	Thr Met	Ile Tyr	Asp Arg Gly	Asn Gly Glu Glu
	450		455		460
Thr Glu Thr	Leu Glu	Asn Gln	Asn Ile	Gln Leu Asp	Leu Lys Lys Val
	465		470		475
Glu Leu Lys	Asn Ile	Lys Arg	Thr Asp	Leu Ile Lys	Tyr Glu Asn Gly
	485		490		495
Lys Glu Thr	Asn Glu	Ser Leu	Ile Thr	Thr Ile Pro	Asp Asp Lys Ser
	500		505		510
Asn Tyr Tyr	Leu Lys	Ile Thr	Ser Asn	Asn Gln Lys	Thr Thr Leu Leu

FOOTNOTES: 012201

525

Lys Phe Glu Glu Glu  
565

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AAACACCTGTA	TATAAAGTTA	CAGCAATCGC	AGACAATTTA	GTCTCTAGAA	CTGCTGATAA	60
TAAATTTGAA	GAAGAATACG	TTCACTATAT	TGAAAAACCT	AAAGTCCACG	AAGATAATGT	120
ATATTATAAT	TTCAAAGAAT	TAGTGGAAGC	TATTCAAAAC	GATCCTTCAA	AAGAATATCG	180
TCTGGGACAA	TCAATGAGCG	CTAGAAATGT	TGTTCTTAAT	GGAAAATCAT	ATATCACTAA	240
AGAATTCACA	GGAAAACTTT	TAAGTTCTGA	AGGAAAACAA	TTTGCTATTA	CTGAATTGGA	300
ACATCCATTA	TTTAATGTGA	TAACAAACGC	AACGATAAAT	AATGTGAATT	TTGAAAATGT	360
AGAGATAGAA	CGTTCTGGTC	AAGATAATAT	TGCATCATT	GCCAATACTA	TGAAAGGTTT	420
TTCAGTTATT	ACAAATGTCA	AAATTACAGG	CACACTTTCA	GGTCGTAATA	ATGTTGCTGG	480
ATTTGTAAAT	AATATGAATG	ATGGAACTCG	TATTGAAAAT	GTTGCTTTCT	TTGGCAAAC	540
ACACTCTACA	AGTGGAATG	GCTCTCATAC	AGGGGGAATT	GCAGGTACAA	ACTATAGAGG	600
AATTGTTAGA	AAAGCATATG	TTGATGCTAC	TATTACAGGA	AACAAAACAC	GCGCCAGCTT	660
GTTAGTTCCT	AAAGTAGATT	ATGGATTAA	TCTAGACCAT	CTTATTGGTA	CAAAGCTCT	720
CCTAACTGAG	TCGGTTGTAA	AAGGTAAAAT	AGATGTTTCA	AATCCAGTAG	AAGTTGGAGC	780
AATAGCAAGT	AAGACTTGGC	CTGTAGGTAC	GGTAAGTAAT	TCTGTCAGCT	ATGCTAAGAT	840
TATCCGTGGA	GAGGAGTTAT	TCGGCTCTAA	CGACGTTGAT	GATTCTGATT	ATGCTAGTGC	900
TCATATAAAA	GATTTATATG	CGGTAGAGGG	ATATTCGTCA	GGTAATAGAT	CATTTAGGAA	960
ATCTAAAACA	TTTACTAAAT	TAATAAAGA	ACAAGCTGAT	GCTAAAGTTA	CTACTTTCAA	1020
TATTACTGCT	GATAAATTAG	AAAGTGATCT	ATCTCCTCTT	GCAAACTTA	ATGAAGAAAA	1080
AGCCTATTCT	AGTATTCAAG	ATTATAACGC	TGAATATAAC	CAAGCCTATA	AAAATCTTGA	1140
AAAATTAATA	CCATTCTACA	ATAAAGATTA	TATTGTATAT	CAAGGTAATA	AATTAAATAA	1200

AGAACACCAT CTAAATACTA AAGAAGTTCT TTCTGTTACC GCGATGAACA ACAATGAGTT 1260  
 TATCACAAAC CTAGATGAAG CTAATAAAAT TATTGTTTAC TATGCGGACG GTACAAAAGA 1320  
 TTACTTTAAC TTGTCTTCTA GCAGTGAAGG TTTAAGTAAT GTAAAAGAAT ATACTATAAC 1380  
 TGACTIONAGGA ATTAAATATA CACCTAATAT CGTTCAAAAA GATAACACTA CTCTTGTTAA 1440  
 TGATATAAAA TCTATTTTAG AATCAGTAGA GCTTCAGTCT CAAACGATGT ATCAGCATCT 1500  
 AAATCGATTA GGTGACTATA GAGTTAATGC AATCAAAGAT TTATATTTAG AAGAAAGCTT 1560  
 CACAGATGTT AAAGAAAACCT TAACAAACCT AATCACAAAA TTAGTTCAAA ACGAAGAACA 1620  
 TCAACTAAAT GATTCTCCAG CTGCTCGTCA AATGATTCGT GATAAAGTCG AGAAAAACAA 1680  
 AGCAGCTTTA TTACTAGGTT TAACTTACCT AAATCGTTAC TATGGAGTTA AATTTGGTGA 1740  
 TGTTAATATT AAAGAATTAA TGCTATTCAA ACCAGATTTT TATGGTGAAA AAGTTAGCGT 1800  
 ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT 1860  
 CGACGCATTC GGTCAAGTA 1879

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Thr	Pro	Val	Tyr	Lys	Val	Thr	Ala	Ile	Ala	Asp	Asn	Leu	Val	Ser	Arg
1				5					10					15	
Thr	Ala	Asp	Asn	Lys	Phe	Glu	Glu	Glu	Tyr	Val	His	Tyr	Ile	Glu	Lys
			20					25					30		
Pro	Lys	Val	His	Glu	Asp	Asn	Val	Tyr	Tyr	Asn	Phe	Lys	Glu	Leu	Val
		35					40					45			
Glu	Ala	Ile	Gln	Asn	Asp	Pro	Ser	Lys	Glu	Tyr	Arg	Leu	Gly	Gln	Ser
	50					55					60				
Met	Ser	Ala	Arg	Asn	Val	Val	Pro	Asn	Gly	Lys	Ser	Tyr	Ile	Thr	Lys
	65				70				75					80	
Glu	Phe	Thr	Gly	Lys	Leu	Leu	Ser	Ser	Glu	Gly	Lys	Gln	Phe	Ala	Ile
			85						90					95	
Thr	Glu	Leu	Glu	His	Pro	Leu	Phe	Asn	Val	Ile	Thr	Asn	Ala	Thr	Ile
		100						105					110		
Asn	Asn	Val	Asn	Phe	Glu	Asn	Val	Glu	Ile	Glu	Arg	Ser	Gly	Gln	Asp
		115					120					125			
Asn	Ile	Ala	Ser	Leu	Ala	Asn	Thr	Met	Lys	Gly	Ser	Ser	Val	Ile	Thr
	130					135						140			

09765272.012201

Asn Val Lys Ile Thr Gly Thr Leu Ser Gly Arg Asn Asn Val Ala Gly  
 145 150 155 160  
 Phe Val Asn Asn Met Asn Asp Gly Thr Arg Ile Glu Asn Val Ala Phe  
 165 170 175  
 Phe Gly Lys Leu His Ser Thr Ser Gly Asn Gly Ser His Thr Gly Gly  
 180 185 190  
 Ile Ala Gly Thr Asn Tyr Arg Gly Ile Val Arg Lys Ala Tyr Val Asp  
 195 200 205  
 Ala Thr Ile Thr Gly Asn Lys Thr Arg Ala Ser Leu Leu Val Pro Lys  
 210 215 220  
 Val Asp Tyr Gly Leu Thr Leu Asp His Leu Ile Gly Thr Lys Ala Leu  
 225 230 235 240  
 Leu Thr Glu Ser Val Val Lys Gly Lys Ile Asp Val Ser Asn Pro Val  
 245 250 255  
 Glu Val Gly Ala Ile Ala Ser Lys Thr Trp Pro Val Gly Thr Val Ser  
 260 265 270  
 Asn Ser Val Ser Tyr Ala Lys Ile Ile Arg Gly Glu Glu Leu Phe Gly  
 275 280 285  
 Ser Asn Asp Val Asp Asp Ser Asp Tyr Ala Ser Ala His Ile Lys Asp  
 290 295 300  
 Leu Tyr Ala Val Glu Gly Tyr Ser Ser Gly Asn Arg Ser Phe Arg Lys  
 305 310 315 320  
 Ser Lys Thr Phe Thr Lys Leu Thr Lys Glu Gln Ala Asp Ala Lys Val  
 325 330 335  
 Thr Thr Phe Asn Ile Thr Ala Asp Lys Leu Glu Ser Asp Leu Ser Pro  
 340 345 350  
 Leu Ala Lys Leu Asn Glu Glu Lys Ala Tyr Ser Ser Ile Gln Asp Tyr  
 355 360 365  
 Asn Ala Glu Tyr Asn Gln Ala Tyr Lys Asn Leu Glu Lys Leu Ile Pro  
 370 375 380  
 Phe Tyr Asn Lys Asp Tyr Ile Val Tyr Gln Gly Asn Lys Leu Asn Lys  
 385 390 395 400  
 Glu His His Leu Asn Thr Lys Glu Val Leu Ser Val Thr Ala Met Asn  
 405 410 415  
 Asn Asn Glu Phe Ile Thr Asn Leu Asp Glu Ala Asn Lys Ile Ile Val  
 420 425 430  
 His Tyr Ala Asp Gly Thr Lys Asp Tyr Phe Asn Leu Ser Ser Ser Ser  
 435 440 445  
 Glu Gly Leu Ser Asn Val Lys Glu Tyr Thr Ile Thr Asp Leu Gly Ile  
 450 455 460  
 Lys Tyr Thr Pro Asn Ile Val Gln Lys Asp Asn Thr Thr Leu Val Asn  
 465 470 475 480

09765272.012201

Asp Ile Lys Ser Ile Leu Glu Ser Val Glu Leu Gln Ser Gln Thr Met  
485 490 495

Tyr Gln His Leu Asn Arg Leu Gly Asp Tyr Arg Val Asn Ala Ile Lys  
500 505 510

Asp Leu Tyr Leu Glu Glu Ser Phe Thr Asp Val Lys Glu Asn Leu Thr  
515 520 525

Asn Leu Ile Thr Lys Leu Val Gln Asn Glu Glu His Gln Leu Asn Asp  
530 535 540

Ser Pro Ala Ala Arg Gln Met Ile Arg Asp Lys Val Glu Lys Asn Lys  
545 550 555 560

Ala Ala Leu Leu Leu Gly Leu Thr Tyr Leu Asn Arg Tyr Tyr Gly Val  
565 570 575

Lys Phe Gly Asp Val Asn Ile Lys Glu Leu Met Leu Phe Lys Pro Asp  
580 585 590

Phe Tyr Gly Glu Lys Val Ser Val Leu Asp Arg Leu Ile Glu Ile Gly  
595 600 605

Ser Lys Glu Asn Asn Ile Lys Gly Ser Arg Thr Phe Asp Ala Phe Gly  
610 615 620

Gln Val  
625

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

ATTAGACAGA TTAATTGAAA TCGGTTCTAA AGAGAACAAC ATTAAAGGTT CACGTACATT	60
CGACGCATTC GGTCAAGTAT TGGCTAAATA TACTAAATCA GGTAATTTAG ATGCATTTTTT	120
AAATTATAAT AGACAATTGT TCACAAATAT AGACAATATG AACGATTGGT TTATTGATGC	180
TACAGAAGAC CATGTCTACA TCGCAGAACG CGCTTCTGAG GTCGAAGAAA TTAAAAATTC	240
TAAACATCGT GCATTCGATA ATTTAAAACG AAGTCACCTT AGAAATACTA TACTCCCACT	300
ACTGAATATT GATAAAGCAC ATCTTTATTT AATTTCAAAT TATAATGCAA TTGCCTTTGG	360
TAGTGCAGAG CGATTAGGTA AAAAATCATT AGAAGATATT AAAGATATCG TTAACAAAGC	420
TGCAGATGGT TATAGAAACT ATTATGATTT CTGGTATCGT CTAGCGTCTG ATAACGTTAA	480
ACAACGACTA CTAAGAGATG CTGTTATTCC TATTTGGGAA GGTATAACG CTCCTGGTGG	540
ATGGGTTGAA AAATATGGCC GCTATAATAC CGACAAAGTA TATACTCCTC TTAGAGAATT	600

09765272.012201

(2) INFORMATION FOR SEQ ID NO:222:

(A) LENGTH: 592 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Asn Ile Asp Asn Met Asn Asp Trp Phe Ile Asp Ala Thr Glu Asp His



50

55

60

Val Tyr Ile Ala Glu Arg Ala Ser Glu Val Glu Glu Ile Lys Asn Ser  
 65 70 75 80  
 Lys His Arg Ala Phe Asp Asn Leu Lys Arg Ser His Leu Arg Asn Thr  
 85 90 95  
 Ile Leu Pro Leu Leu Asn Ile Asp Lys Ala His Leu Tyr Leu Ile Ser  
 100 105 110  
 Asn Tyr Asn Ala Ile Ala Phe Gly Ser Ala Glu Arg Leu Gly Lys Lys  
 115 120 125  
 Ser Leu Glu Asp Ile Lys Asp Ile Val Asn Lys Ala Ala Asp Gly Tyr  
 130 135 140  
 Arg Asn Tyr Tyr Asp Phe Trp Tyr Arg Leu Ala Ser Asp Asn Val Lys  
 145 150 155 160  
 Gln Arg Leu Leu Arg Asp Ala Val Ile Pro Ile Trp Glu Gly Tyr Asn  
 165 170 175  
 Ala Pro Gly Gly Trp Val Glu Lys Tyr Gly Arg Tyr Asn Thr Asp Lys  
 180 185 190  
 Val Tyr Thr Pro Leu Arg Glu Phe Phe Gly Pro Met Asp Lys Tyr Tyr  
 195 200 205  
 Asn Tyr Asn Gly Thr Gly Ala Tyr Ala Ala Ile Tyr Pro Asn Ser Asp  
 210 215 220  
 Asp Ile Arg Thr Asp Val Lys Tyr Val His Leu Glu Met Val Gly Glu  
 225 230 235 240  
 Tyr Gly Ile Ser Val Tyr Thr His Glu Thr Thr His Val Asn Asp Arg  
 245 250 255  
 Ala Ile Tyr Leu Gly Gly Phe Gly His Arg Glu Gly Thr Asp Ala Glu  
 260 265 270  
 Ala Tyr Ala Gln Gly Met Leu Gln Thr Pro Val Thr Gly Ser Gly Phe  
 275 280 285  
 Asp Glu Phe Gly Ser Leu Gly Ile Asn Met Val Phe Lys Arg Lys Asn  
 290 295 300  
 Asp Gly Asn Gln Trp Tyr Ile Thr Asp Pro Lys Thr Leu Lys Thr Arg  
 305 310 315 320  
 Glu Asp Ile Asn Arg Tyr Met Lys Gly Tyr Asn Asp Thr Leu Thr Leu  
 325 330 335  
 Leu Asp Glu Ile Glu Ala Glu Ser Val Ile Ser Gln Gln Asn Lys Asp  
 340 345 350  
 Leu Asn Ser Ala Trp Phe Lys Lys Ile Asp Arg Glu Tyr Arg Asp Asn  
 355 360 365  
 Asn Lys Leu Asn Gln Trp Asp Lys Ile Arg Asn Leu Ser Gln Glu Glu  
 370 375 380  
 Lys Asn Glu Leu Asn Ile Gln Ser Val Asn Asp Leu Val Asp Gln Gln

09765272.012201

385		390		395		400
Leu Met Thr Asn Arg Asn Pro Gly Asn Gly Ile Tyr Lys Pro Glu Ala						
	405			410		415
Ile Ser Tyr Asn Asp Gln Ser Pro Tyr Val Gly Val Arg Met Met Thr						
	420		425		430	
Gly Ile Tyr Gly Gly Asn Thr Ser Lys Gly Ala Pro Gly Ala Val Ser						
	435		440		445	
Phe Lys His Asn Ala Phe Arg Leu Trp Gly Tyr Tyr Gly Tyr Glu Asn						
	450		455		460	
Gly Phe Leu Gly Tyr Ala Ser Asn Lys Tyr Lys Gln Gln Ser Lys Thr						
	465		470		475	480
Asp Gly Glu Ser Val Leu Ser Asp Glu Tyr Ile Ile Lys Lys Ile Ser						
	485		490		495	
Asn Asn Thr Phe Asn Thr Ile Glu Glu Phe Lys Lys Ala Tyr Phe Lys						
	500		505		510	
Glu Val Lys Asp Lys Ala Thr Lys Gly Leu Thr Thr Phe Glu Val Asn						
	515		520		525	
Gly Ser Ser Val Ser Ser Tyr Asp Asp Leu Leu Thr Leu Phe Lys Glu						
	530		535		540	
Ala Val Lys Lys Asp Ala Glu Thr Leu Lys Gln Glu Ala Asn Gly Asn						
	545		550		555	560
Lys Thr Val Ser Met Asn Asn Thr Val Lys Leu Lys Glu Ala Val Tyr						
	565		570		575	
Lys Lys Leu Leu Gln Gln Thr Asn Ser Phe Lys Thr Ser Ile Phe Lys						
	580		585		590	

## (2) INFORMATION FOR SEQ ID NO: 223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

TAAGACAGAT GAACGGAGCA AGGTGTTTGA CTTTTCATT CCCTACTATA CTGCAAAAAA	60
TAAACTCATT GTCAAAAAT CTGACTTGAC TACTTATCAG TCTGTAAACG ACTTGGCGCA	120
GAAAAAGGTT GGAGCGCAGA AAGGTCGAT TCAAGAGACG ATGGCGAAAG ATTTGCTACA	180
AAATTCTTCC CTCGTATCTC TGCCTAAAAA TGGAATTTA ATCACAGATT TAAATCAGG	240
ACAAGTGGAT GCCGTTATCT TTGAAGAACC TGTTTCCAAG GGATTTGTGG AAAATAATCC	300
TGATTTAGCA ATCGCAGACC TCAATTTTGA AAAAGAGCAA GATGATTCCT ACGCGGTAGC	360
CATgAAAAAA GATAGCAAGA AATTGAAGAG GCAGTTCGAT AAAACCATTC AAAAGTTGAA	420

09765272.012201

GGAGTCTGGG GAATTAGACA AACTCATTGA GGAAGCCTTA

460

## (2) INFORMATION FOR SEQ ID NO:224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

Lys Thr Asp Glu Arg Ser Lys Val Phe Asp Phe Ser Ile Pro Tyr Tyr
1          5          10          15
Thr Ala Lys Asn Lys Leu Ile Val Lys Lys Ser Asp Leu Thr Thr Tyr
          20          25          30
Gln Ser Val Asn Asp Leu Ala Gln Lys Lys Val Gly Ala Gln Lys Gly
          35          40          45
Ser Ile Gln Glu Thr Met Ala Lys Asp Leu Leu Gln Asn Ser Ser Leu
          50          55          60
Val Ser Leu Pro Lys Asn Gly Asn Leu Ile Thr Asp Leu Lys Ser Gly
          65          70          75          80
Gln Val Asp Ala Val Ile Phe Glu Glu Pro Val Ser Lys Gly Phe Val
          85          90          95
Glu Asn Asn Pro Asp Leu Ala Ile Ala Asp Leu Asn Phe Glu Lys Glu
          100          105          110
Gln Asp Asp Ser Tyr Ala Val Ala Met Lys Lys Asp Ser Lys Lys Leu
          115          120          125
Lys Arg Gln Phe Asp Lys Thr Ile Gln Lys Leu Lys Glu Ser Gly Glu
          130          135          140
Leu Asp Lys Leu Ile Glu Glu Ala Leu
          145          150

```

## (2) INFORMATION FOR SEQ ID NO: 225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

```

CTGTGAGAAT CAAGCTACAC CCAAAGAGAC TAGCGCTCAA AAGACAATCG TCCTTGCTAC      60
AGCTGGCGAC GTGCCACCAT TTGACTACGA AGACAAGGGC AATCTGACAG GCTTTGATAT      120
CGAAGTTTTA AAGGCAGTAG ATGAAAAACT CAGCGACTAC GAGATTCAAT TCCAAAGAAC      180

```

09765272.012201

CGCCTGGGAG AGCATCTTCC CAGGACTTGA TTCTGGTCAC TATCAGGCTG CGGCCAATAA 240  
 CTTGAGTTAC ACAAAGAGC GTGCTGAAAA ATACCTTTAC TCGCTTCCAA TTTCCAACAA 300  
 TCCCCTCGTC CTTGTCAGCA ACAAGAAAAA TCCTTTGACT TCTCTTGACC AGATCGCTGG 360  
 TAAAACAACA CAAGAGGATA CCGGAAC TTC TCAACGCTCAA TTCATCAATA ACTGGAATCA 420  
 GAAACACACT GATAATCCCG CTACAATTAA TTTTCTGGT GAGGATATTG GTAAACGAAT 480  
 CCTAGACCTT GCTAACGGAG AGTTTGATTT CCTAGTTTTT GACAAGGTAT CCGTTCAAAA 540  
 GATTATCAAG GACCGTGGTT TAGACCTCTC AGTCGTTGAT TTACCTTCTG CAGATAGCCC 600  
 CAGCAATTAT ATCATTTTCT CAAGCGACCA AAAAGAGTTT AAAGAGCAAT TTGATAAAGC 660  
 GCTCAAAGAA CTCTATCAAG ACGGAACCCT TGAAAACTC AGCAATACCT ATCTAGGTGG 720  
 TTCTTACCTC CCAGATCAAT CTCAGTTACA A 751

## (2) INFORMATION FOR SEQ ID NO:226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Cys	Glu	Asn	Gln	Ala	Thr	Pro	Lys	Glu	Thr	Ser	Ala	Gln	Lys	Thr	Ile	1	5	10	15
Val	Leu	Ala	Thr	Ala	Gly	Asp	Val	Pro	Pro	Phe	Asp	Tyr	Glu	Asp	Lys	20	25	30	
Gly	Asn	Leu	Thr	Gly	Phe	Asp	Ile	Glu	Val	Leu	Lys	Ala	Val	Asp	Glu	35	40	45	
Lys	Leu	Ser	Asp	Tyr	Glu	Ile	Gln	Phe	Gln	Arg	Thr	Ala	Trp	Glu	Ser	50	55	60	
Ile	Phe	Pro	Gly	Leu	Asp	Ser	Gly	His	Tyr	Gln	Ala	Ala	Ala	Asn	Asn	65	70	75	80
Leu	Ser	Tyr	Thr	Lys	Glu	Arg	Ala	Glu	Lys	Tyr	Leu	Tyr	Ser	Leu	Pro	85	90	95	
Ile	Ser	Asn	Asn	Pro	Leu	Val	Leu	Val	Ser	Asn	Lys	Lys	Asn	Pro	Leu	100	105	110	
Thr	Ser	Leu	Asp	Gln	Ile	Ala	Gly	Lys	Thr	Thr	Gln	Glu	Asp	Thr	Gly	115	120	125	
Thr	Ser	Asn	Ala	Gln	Phe	Ile	Asn	Asn	Trp	Asn	Gln	Lys	His	Thr	Asp	130	135	140	
Asn	Pro	Ala	Thr	Ile	Asn	Phe	Ser	Gly	Glu	Asp	Ile	Gly	Lys	Arg	Ile	145	150	155	160

09765272.012201

Leu Asp Leu Ala Asn Gly Glu Phe Asp Phe Leu Val Phe Asp Lys Val  
 165 170 175

Ser Val Gln Lys Ile Ile Lys Asp Arg Gly Leu Asp Leu Ser Val Val  
 180 185 190

Asp Leu Pro Ser Ala Asp Ser Pro Ser Asn Tyr Ile Ile Phe Ser Ser  
 195 200 205

Asp Gln Lys Glu Phe Lys Glu Gln Phe Asp Lys Ala Leu Lys Glu Leu  
 210 215 220

Tyr Gln Asp Gly Thr Leu Glu Lys Leu Ser Asn Thr Tyr Leu Gly Gly  
 225 230 235 240

Ser Tyr Leu Pro Asp Gln Ser Gln Leu Gln  
 245 250

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

GACTGGATCC TAAATCTAC GACAATAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

CTGAGTCGAC TGGTTGTGCT GGTGAG

27

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

GTCAGGATCC AAATTACAAT ACGGACTATG

30

(2) INFORMATION FOR SEQ ID NO: 230:

00765272.012201

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CAGTGTCTGAC TAACTCTAGG TCGGAAAC

28

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GACTGGATCC TGAGAATCAA GCTACACCCA AAGAG

35

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGTCAAGCTT TTGTAAGTGA GATTGATCTG G

31

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GACTGGATCC TGGTAACCGC TCTTCTCGTA ACGCAGC

37

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

00765272.012201  
 102210 2259760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

AGTCAAGCTT TTTCAGGAAC TTTTACGCTT CC

32

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

AGTCAGATCT TGTGGAAATT TGACAGGTAA CAGCAAAAAA GCTGC

45

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

ACTGAAGCTT TTTTGT TTTT CAAGAATTCA TCG

33

(2) INFORMATION FOR SEQ ID NO: 237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

GACTGGATCC TGGTCAAGGA ACTGCTTCTA AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

AGTCAAGCTT TCACAAATTC GTTGGTGAAG CC

32

(2) INFORMATION FOR SEQ ID NO: 239:

00765272.012201

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

GACTGGATCC TAGCTCAGGT GGAAACGCTG GTTCATCC

38

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

AGTCAAGCTT ATCAACTTTT CCACCTTCAA CAACC

35

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

GTCAAGATCT CTCCAACATAT GGTAAATCTG CGGATGG

37

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

AGTCCTGCAG ATCCACATCC GCTTTCATCG GGTAAAGAA GG

42

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

0076527.012201



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

GACTGGATCC TGGGAAAAAT TCTAGCGAAA CTAGTGG

37

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

GTCAGTGCAG CTGTCCTTCT TTTACTTCTT TGGTTGC

37

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

GACTGGATCC TGCTAGCGGA AAAAAAGATA CAACTTCTGG

40

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

CTGAAAGCTT TTTTGCCAAT CCTTCAGCAA TCTTGTC

37

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

GACTAGATCT TGGCTCAAAA AATACAGCTT CAAGTCC

37

(2) INFORMATION FOR SEQ ID NO: 248:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

AGTCCTGCAG GTTTTTGTTT GCTTGGTATT GGTCG

35

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

GACTGGATCC TAGTACAAAC TCAAGCACTA GTCAGACAGA G

41

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CAGTCTGCAG TTTCAAAGCT TTTTGTATGT CTTC

34

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

GACTGGATCC TGGCAATTCT GCGGAAGTA AAGATGC

37

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765272.012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

AGTCAAGCTT GTTTCATAGC TTTTGTGATT GTTTCG

36

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

GACTGGATCC TTCACAAGAA AAAACAAAAA ATGAAGATGG

40

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

AGTCAAGCTT ATCGACGTAG TCTCCGCCTT C

31

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

GACTGGATCC GAAAGGTCTG TGGTCAAATA ATCTTACC

38

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

AGTCAAGCTT AGAGTTAACA TGGTGCTTGC CAATAGG

37

(2) INFORMATION FOR SEQ ID NO: 257:

00765272.012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GACTGGATCC AAACTCAGAA AAGAAAGCAG ACAATGC

37

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGTCAAGCTT CCAAAGCTGGT TGATCCAAAC CATCTG

36

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

GACTGGATCC TTCGAAAGGG TCAGAAGGTG CAGACC

36

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AGTCAAGCTT CTGTAGGCTT GGTGTGCCCC AGTTGC

36

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765272-012204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTGAGGATCC GGGGATGGCA GCTTTTAAAA ATC

33

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CAGTAAGCTT GTTTACCCAT TCACCATTAC C

31

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CAGTGGATCC AGACGAGCAA AAAATTAAG

29

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TCAGAAGCTT GTTTACCCAT TCACCATT

28

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

GACTGGATCC CTGTGGTGAG GAAGAACTA AAAAG

35

(2) INFORMATION FOR SEQ ID NO: 266:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

CTGAGTCGAC AATATTCTGT AGGAATGCTT CGAATTTG

38

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

CTGAGGATCC GACTTTTAAC AATAAACTA TTGAAGAG

38

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

GTCAGTGCAG GTTGTCACCT CCAAAAATCA CGG

33

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GACTGGATCC CTTTACAGGT AAACAACTAC AAGTCGG

37

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

09765272-012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

CAGTAAGCTT TTCGAAGTTT GGCTCAGAAT TG

32

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

GACTGGATCC CCAGGCTGAT ACAAGTATCG CA

32

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CAGTAAGCTT ATCTGCAGTA TGGCTAGATG G

31

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

GACTGGATCC GTCTGTATCA TTTGAAAACA AAGAAAC

37

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CAGTCTGCAG TTTTACTGTT GCTGTGCTTG TG

32

(2) INFORMATION FOR SEQ ID NO: 275:

09765272-012201

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ACTGAGATCT TGGTCAAAAG GAAAGTCAGA CAGGAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGTAAGCTT ATTCTGAGC TTTTGTGATA AAGGTTGCGC A

41

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

ACTGGGATCC GAAGGATAGA TATATTTTAG CATTTGAGAC

40

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AGTCAAGCTT CCATGGTATC AAAGGCAAGA CTTGG

35

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765272-012201



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

GTCAGGATCC GGTAGTTAAA GTTGGTATTA ACGG

34

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

AGTCAAGCTT GCAATTTTGG CGAAGTATTC CAAGAG

36

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

AGTCGGATCC TTCTTACGAG TTGGGACTGT ATCAAGC

37

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

AGTCAAGCTT GTTTATTTTT TCCTTACTTA CAGATGAAGG

40

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

AGTCGGATCC TACTGAGATG CATCATAATC TAGGAGC

37

(2) INFORMATION FOR SEQ ID NO: 284:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

TCAGCTCGAG TTCTTTGACA TCTCCATCAT AAGTCGC

37

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

GACTGGATCC GGTTTTGAGA AAGTATTTGC AGGGG

35

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

CAGTAAGCTT GGATTTTTTC ATGGATGCAA TTTTTTTGG

39

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GACTGGATCC GACAACATTT ACTATCCATA CAGTAGAGTC AGC

43

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

00765272.012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

GACTAAGCTT GGCATAAGGT TGCAATTCTG GATTAATTGG

40

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

GACTGGATCC GGCTAAGGAA AGAGTGGATG

30

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GACTAAGCTT TTCATTTTAA AATTGACTAT GCGCCCCG

37

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

GACTGGATCC TTGTTCTAT GAACTTGGTC GTCACC

36

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CATGAAGCTT ATCCTGGATT TTTCCAAGTA AATCT

35

(2) INFORMATION FOR SEQ ID NO: 293:

09765272.012204

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

GACTGGATCC TTATAAGGGT GAATTAGAAA AAGG

34

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

GACTAAGCTT CTTATTAGGA TTGTTAGTAG TTG

33

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

GACTGGATCC GAATGTTCAG GCTCAAGAAA GTTCAGG

37

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GACTAAGCTT TTCCCCTGAT GGAGCAAAGT AATACC

36

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09/09/92 10:22:01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

GACTGGATCC CTTGGGTGTA ACCCATATCC AGCTCCTTCC

40

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GACTGTCGAC TTCAGCTTGT TTATCTGGGG TTGC

34

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GACTGGATCC TAGTGATGGT ACTTGGCAAG GAAAACAG

38

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

ACTGCTGCAG ATCTTTGCCA CCTAGCTTCT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

GTCAGGATCC TGGGATTCAA TATGTCAGAG ATGATACTAG

40

(2) INFORMATION FOR SEQ ID NO: 302:

097655272.012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

CTAGAAGCTT ACGCACCCAT TCACCATTAT CATTG

35

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

GTCAGGATCC GGATAATAGA GAAGCATTAA AAACC

35

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AGTCAAGCTT GACAAAATCT TGAAACTCCT CTGGTC

36

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GTCAGGATCC AGATTTTGTC GAGGAGTGTC ATACC

35

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765272-012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

AGTCAAGCTT TCCCTTTTTA CCCTTACGAA TCCAGG

36

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GACTGGATCC ATCTGTAGTT TATGCGGATG AAACACTTAT TAC

43

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

GACTGTCGAC GCTTTGGTAG AGATAGAAGT CATG

34

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

GACTGGATCC TTA CTTTGGT ATCGTAGATA CAGCCGGC

38

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AGTCAAGCTT TGTTAATTGC GTACCTTCTA AGCGACC

37

(2) INFORMATION FOR SEQ ID NO: 311:

09765272:012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GACTGGATCC AGCTAAGGTT GCATGGGATG CGATTCG

37

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

GACTGTCGAC CTGGGCTTTA TTAGTTTGAC TAGC

34

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

CAGTGGATCC CTATCACTAT GTAAATAAAG AGA

33

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

ACTGAAGCTT TTCTGTCCCT GTTTGAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765272.012201



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

CAGTGGATCC TGAGACTCCT CAATCAATAA CAAA

34

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

ACGTAAGCTT ATAATCAGTA GGAGAACTG AACT

34

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CAGTGGATCC GGATGCTCAA GAAACTGCGG

30

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

GACTAAGCTT TTGCTCTCA TTCTTGCTTC C

31

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

CAGTGGATCC CGACAAAGGT GAGACTGAG

29

(2) INFORMATION FOR SEQ ID NO: 320:

09765272 012201

- (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

ACGTAAGCTT ATTTCTTAAT TCAAGTGTTT TCTCTG

36

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double.  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GACTGGATCC AAATCAATTG GTAGCACAAG ATCC

34

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CAGTGTCGAC ATTAGGAGCC ACTGGTCTC

29

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

CAGTGGATCC CAAACAGTCA GCTTCAGGAA C

31

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

GACTCTGCAG TTTAATCTTG TCCCAGGTGG

30

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

GACTGGATCC ATTCGATGAT GCGGATGAAA AG

32

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

GACTAAGCTT CATTTGTCTT TGGGTATTTT GCA

33

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

CAGTGGATCC GGAGAGTCGA TCAAAAGTAG

30

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GTCAGTGCAG TTGCTCGTCT CGAGGTTC

28

(2) INFORMATION FOR SEQ ID NO: 329:

09765272-012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

CAGTGGATCC ATGGACAACA GGAAACTGGG AC

32

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

CAGTAAGCTT ATTAGCTTCT GTACCTGTGT TTG

33

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

GACTGGATCC CGATGGGCTC AATCCAACCC CAGGTCAAGT C

41

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GACTCTGCAG CATAGCTTTA TCCTCTGACA TCATCGTATC

40

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765272.012204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

GACTGGATCC TTCCAATCAA AAACAGGCAG ATGG

34

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

GACTAAGCTT GAGTCCCATA GTCCAAGGCA

30

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

AGTCGGATCC TATCACAGGA TCGAACGGTA AGACAACC

38

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

ACTGGTCGAC TTCTTTTAAC TCCGCTACTG TGTC

34

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CAGTGGATCC AAGTTCATCG AAGATGGTTG GGAAGTCC

38

(2) INFORMATION FOR SEQ ID NO: 338:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GATCGTCGAC CCGCTCCAC ATGCTCAACC TT

32

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

TGACGGATCC ATCGCTAGCT AGTGAAATGC AAGAAAG

37

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

TGACAAGCTT ATTCGTTTTT GAACTAGTTG CTTTCGT

37

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GACTGGATCC GCACCAGATG GGGCACAAGG TTCAGGG

37

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765272.012204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

TGACAAGCTT AACTTGTAAC GAACAGTTCA ATCTG

35

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GACTAGATCT TTTTAACCCA ACTGTTGGTA CTTTCC

36

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TGACAAGCTT GTTAGGTGTT ACATTTTGAC CGTC

34

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

ACTGAGATCT TTTTAACCCA ACTGTTGGTA CTTTC

35

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

GACTAAGCTT TCTACGATAA CGATCATTTT CTTTACC

37

(2) INFORMATION FOR SEQ ID NO: 347:

09765272.012201

(i) SEQUENCE CHARACTERISTICS:

- \_\_\_\_ (A) LENGTH: 38 base pairs
- \_\_\_\_ (B) TYPE: nucleic acid
- \_\_\_\_ (C) STRANDEDNESS: double
- \_\_\_\_ (D) TOPOLOGY: linear

GACTGTCGAC TCGTAGATAT TTAAGTCTAA GTGAAGCG

(2) INFORMATION FOR SEQ ID NO: 348:

(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

AGTCAAGCTT GTTAGGTGTT ACATTTTGCA AGTC

(2) INFORMATION FOR SEQ ID NO: 349:

(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

GACTGGATCC CTTTGGTTTT GAAGGAAGTA AG

(2) INFORMATION FOR SEQ ID NO: 350:

(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TGACCTGCAG ACGATTTTGT AAAAATGGAG GTGTATC

(2) INFORMATION FOR SEQ ID NO: 351:

(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

CAGTGGATCC CTACTACCTC TCGAGAGAAA G

31

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

ACTGAAGCTT TTCGCTTTTT ACTCGTTTGA CA

32

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CAGTGGATCC TAAGGTCAAA AGTCAGACCG CTAAGAAAGT GC

42

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

CAGTAAGCTT TAGGGTATCC AAATACTGGT TGTTGATG

38

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TGACAGATCT TGACGGGTCT CAGGATCAGA CTCAGG

36

(2) INFORMATION FOR SEQ ID NO: 356:

09765272.012201

- (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

TGACAAGCTT CAAAGACATC CACCTCTTGA CCTTTG

36

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEOUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

GACTGGATCC TAGAGGCTTT GCCAAATGGT GGGAAGGG

38

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GTCAGTCGAC TTGTTGTAAC ACTTTTCGAG GTTTGGTACC

40

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CAGTGGATCC TCAAAAAGAG AAGGAAAAC TGG

33

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CAGTCTGCAG TTTCTTCAAC AACCTTGTT CTTG

34

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

CAGTGGATCC ACGTTCTATT GAGGACCACT T

31

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

CAGTAAGCTT TTCCTTCTCA GTCAATTCTT TTCC

34

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GACTGGATCC CGCTCAAAAT ACCAGAGGTG TTCAG

35

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

GACTAAGCTT AGTACCATGG GTGTGACAGG TTTGAA

36

(2) INFORMATION FOR SEQ ID NO: 365:

09765272 1012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

CTGAGGATCC AATTGTACAA TTAGAAAAAG ATAGC

35

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

TGACAAGCTT GCGTTGACTA GGTTC TGCAA TGCC

34

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

GACTGGATCC TCTGACCAAG CAAAAGAAG CAGTCAATGA

40

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

TCAGCAGCTG ATCATTGACT TTACGATTTG CTCC

34

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765022.012204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

GACTGGATCC GTCCGGCTCT GTCCAGTCCA CTTTTTCAGC G

41

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAGAAGCTT ATTTTTTGTT TCCTTAATGC GTT

33

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

GACTGGATCC GGGACAAATT CAAAAAATA GGCAAGAGG

39

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

GTCAAAGCTT TGGCTCTTTG ATTGCCAACA ACTG

34

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GACTGGATCC TCGCTACCAG CAACAAAGCG AGCAAAAGG

39

(2) INFORMATION FOR SEQ ID NO: 374:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

GACTAAGCTT ACTTTTTTCT TTTTCCACAC GA

32

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

CAGTGGATCC GAACCGACAA GTCGCCCACT ATCAAGACT

39

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CTGAAAGCTT TGAATTCTCT TTCTTTTCAG GCT

33

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

TCGAGGATCC GGTGTGCGGC TGGCAATATA TCCCGT

36

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

0976527.01201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CAGTAAGCTT CCGAACCCAT TCGCCATTAT AGTTGAC

37

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

AGTCGGATCC GGCCAAATCA GAATGGGTAG AAGAC

35

(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

TGACCTGCAG CTTCTCATTG ATTTTCATCA TCAC

34

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACTGGATCC ATTTGCAGAT GATTCTGAAG GATGG

35

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

TCAGCTGCAG-CTTAACCCAT TCACCATTCT AGTTTAAG

38

(2) INFORMATION FOR SEQ ID NO: 383:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

GACTGGATCC TGTCGCTGCA AATGAACTG AAGTAGC

37

(2) INFORMATION FOR SEQ ID NO: 384:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

GACTAAGCTT ATACCAAACG CTGACATCTA CGCG

34

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

AGTCAGATCT TACGTCTCAG CCTACTTTTG TAAGAGC

37

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

GACTAAGCTT AACCCATTCA CCATTGGCAT TGAC

34

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

0976527-01201



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

CAGTGGATCC TGGACAGGTG AAAGGTCATG CTACATTTGT G

41

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

GACTAAGCTT CAACCATTGA GACCTTGCAA CAC

33

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GTCAGGATCC GATTGCTCCT TTGAAGGATT TGAGAGAAAC C

41

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GACTAAGCTT CGATCAAAGA TAAGATAAAT ATATATAAAG T

41

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GACTGGATCC TAGGTCATAT GGGACTTTTT TTCTACAACA-AAATAGG-----

47

(2) INFORMATION FOR SEQ ID NO: 392:

00765272.012204

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TGACAAGCTT ATCTATCAGC TCATTTAATC GTTTTTG

37

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CTGAGGATCC CAACGTTGAG AATTATTTGC GAATG

35

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

TGACAAGCTT GAGTCTACAA AAGTAATGTA C

31

(2) INFORMATION FOR SEQ ID NO: 395:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

GTCAGGATCC CTACTATCAA TCAAGTTCTT CAGCC

35

(2) INFORMATION FOR SEQ ID NO: 396:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

0075272 012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

TGACAAGCTT GACTGAGGCT TGGACCAGAT TGAAAAG

37

(2) INFORMATION FOR SEQ ID NO: 397:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

GACTGGATCC GACAAAAACA TTAAACGTC CTGAGG

36

(2) INFORMATION FOR SEQ ID NO: 398:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

GACTAAGCTT AGCACGAAC GTGACGCTGG TTCC

34

(2) INFORMATION FOR SEQ ID NO: 399:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

GACTGGATCC TTCTCAGGAG ACCTTTAAAA ATATC

35

(2) INFORMATION FOR SEQ ID NO: 400:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

GACTAAGCTT GTTGGCCATC TTGTACATAC C

31

(2) INFORMATION FOR SEQ ID NO: 401:

09765272.012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 37

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 32

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 32

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

GACTGGATCC GTGGATGGGC TTAACTATC TTCGTATTCTG

40

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

AGTCAAGCTT GCTAGTCTTC ACTTTCCTT TCC

33

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

GACTGTCGAC ACTAAACCAG CATCGTTCGC AGGA

34

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

CTGACTGCAG CTTCTTGAAG AAATAATGAT TGTGG

35

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

CAGTGGATCC TGACTACCTT GAAATCCCAC TT

32

(2) INFORMATION FOR SEQ ID NO: 410:

09765272 012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

CAGTAAGCTT TTTTSTAAGG TTGTAGAATG ATTTCAATC

39

(2) INFORMATION FOR SEQ ID NO: 411:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

CAGTGTGAC TCGTATCTTT TTTTGGAGCA ATGTT

35

(2) INFORMATION FOR SEQ ID NO: 412:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

GACTAAGCTT AAATGTTCCG ATACGGGTGA TTG

33

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

CAGTGGATCC GGACTCTCTC AAAGATGTGA AAG

33

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

097655272.012204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

GACTAAGCTT CTTGAGTTTG TCAAGGATTG CTTT

34

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

CAGTGGATCC CAAGAAATCC TATCATCTCT TCCAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GACTAAGCTT TTCAGAACTA AAAGCCGCAG CTT

33

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

GACTGGATCC ACGAAATGCA GGGCAGACAG

30

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

-----CAGTAAGCTT ATCAACATAA TCTAGTAAAT AAGCGT

36

(2) INFORMATION FOR SEQ ID NO: 419:

00765272.012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

CAGTGGATCC TGTATAGTTT TTAGCGCTTG TTCTTC

36

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GTCAAAGCTT TGATAGAGTG TCATAATCTT CTTTAG

36

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

GACTGGATCC GTGTGTCGAG CATATTCTGA AG

32

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CAGTAAGCTT ACTTTTACCA TTTCTTTGTT CTGCATC

37

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

09765272.012201



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

GACTGTCGAC GTGTTTGGAT AGCATTTCAGA ATCAGACG

38

(2) INFORMATION FOR SEQ ID NO: 424:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

CAGTAAGCTT CGGAAGTAAA GACAATTTTT CC

32

(2) INFORMATION FOR SEQ ID NO: 425:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

CAGTGGATCC GTGCCTAGAT AGTATTATTA CTCAAAC

37

(2) INFORMATION FOR SEQ ID NO: 426:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

GACTAAGCTT TTTGCTTATT TCTCTCAATT TTTC

34

(2) INFORMATION FOR SEQ ID NO: 427:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

CAGTGGATCC CATTTCAGAAG CAGACCTATC-AAAATC

36

(2) INFORMATION FOR SEQ ID NO: 428:

097655272 012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

ACTGAAGCTT ATGTAATTTT TTAGATTTT CAATATTTT CAG

43

(2) INFORMATION FOR SEQ ID NO: 429:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AGTCGGATCC TAAGGCTGAT AATCGTGTTT AAATG

35

(2) INFORMATION FOR SEQ ID NO: 430:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GACTAAGCTT AAAATTAGAT AGACGTTGAG T

31

(2) INFORMATION FOR SEQ ID NO: 431:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

AGTCGGATCC CTGTGGCAAT CAGTCAGCTG CTTCC

35

(2) INFORMATION FOR SEQ ID NO: 432:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

096527012201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

GACTGTCGAC TTTAATCTTG TCCCAGGTGG TTAATTTGCC

40

(2) INFORMATION FOR SEQ ID NO: 433:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

ACTGGTCGAC TTGTCAACAA CAACATGCTA CTTCTGAG

38

(2) INFORMATION FOR SEQ ID NO: 434:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

GACTCTGCAG AAGTTTAACC CACTTATCAT TATCC

35

(2) INFORMATION FOR SEQ ID NO: 435:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

ACTGGGATCC TTGTTCAAGC AAGTCCGTGA CTAGTGAAC

39

(2) INFORMATION FOR SEQ ID NO: 436:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

GACTAAGCTT GGCTAATTCC TTCAAAGTTT GCA

33

(2) INFORMATION FOR SEQ ID NO: 437:

0965272.012201

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

AGTCGGATCC CTCGCAAATT GAAAAGGCGG CAGTTAGCC

39

(2) INFORMATION FOR SEQ ID NO: 438:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

GACTAAGCTT GTAAATAAGC GTACCTTTTT CTTC

35

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

TCAGGGATCC TTGTCAGTCA GGTCTAATG GTTCTCAG

38

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

AGTCAAGCTT GGCATTGGCG TCGCCGTCCT TC

32

(2) INFORMATION FOR SEQ ID NO: 441:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

0965372 012301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

GACTGGATCC GGAAACTTCA CAGGATTTTA AAGAGAAG

38

(2) INFORMATION FOR SEQ ID NO: 442:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

GACTGTCGAC AATCAATCCT TCTTCTGCAC TTCT

34

(2) INFORMATION FOR SEQ ID NO: 443:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

CAGTGGATCC TGTGGTCGAA GTTGAGACTC CTCAATC

37

(2) INFORMATION FOR SEQ ID NO: 444:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

GACTAAGCTT TTCTTCAAAT TTATTATCAG C

31

(2) INFORMATION FOR SEQ ID NO: 445:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

AGTCGGATCC AACACCTGTA TATAAAGTTA CAGCAATCG

39

(2) INFORMATION FOR SEQ ID NO: 446:

09765272.012201

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

GACTGTCGAC TACTTGACCG AATGCGTCGA ATGTACG

37

(2) INFORMATION FOR SEQ ID NO: 447:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

CTGAGGATCC ATTAGACAGA TTAATTGAAA TCGG

34

(2) INFORMATION FOR SEQ ID NO: 448:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

GACTGTCGAC TTAAAGATT GAAGTTTAA AGCT

34

(2) INFORMATION FOR SEQ ID NO: 449:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

TGACGGATCC TAAGACAGAT GAACGGAGCA AGGTG

35

(2) INFORMATION FOR SEQ ID NO: 450:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

0965272 012201

